

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2004, 16:20:08 ; Search time 60 Seconds

(without alignments)
998.335 Million cell updates/sec

Title: US-09-997-641-387

Perfect score: 1102
Sequence: 1 MLWLLFFLVTAHAEACQPG.....ENGIPSDPLDMKGILWMP5 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1990s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1102	100.0	212	3	AAY66751 Membrane-
2	1102	100.0	212	3	AAB33447 Human PRO
3	1102	100.0	212	3	AAB24430 Human PRO
4	1102	100.0	212	4	AAL12412 Human PRO
5	1102	100.0	212	4	AAB52274 Human PRO
6	1102	100.0	212	6	ABU58089 Human PRO
7	1102	100.0	212	6	ABU59167 Novel hum
8	1102	100.0	212	6	ABU82679 Human sec
9	1102	100.0	212	6	ABO17856 Novel hum
10	1102	100.0	212	6	ABU60598 Human sec
11	1102	100.0	212	6	ABU13980 Human PRO
12	1102	100.0	212	6	ABU81110 Human PRO
13	1102	100.0	212	6	ABU72565 Novel hum
14	1102	100.0	212	6	ABU66810 Human PRO
15	1102	100.0	212	6	ABU59891 Novel sec
16	1102	100.0	212	6	ABU59314 Human sec
17	1102	100.0	212	6	ABO26011 Human PRO
18	1102	100.0	212	6	ABO25081 Human sec
19	1102	100.0	212	6	ABU59020 Human sec
20	1102	100.0	212	6	ABU92398 Novel hum
21	1102	100.0	212	6	ABU59463 Novel hum
22	1102	100.0	212	6	ABU67086 Human sec
23	1102	100.0	212	6	ABU92229 Novel hum
24	1102	100.0	212	6	ABU10935 Human PRO
25	1102	100.0	212	6	ABU81687 Novel hum

ALIGNMENTS

RESULT 1
AAY66751
ID AAY66751 standard; protein; 212 AA.
XX

AC AAY66751;

DT 05-APR-2000 (first entry)

XX Membrane-bound protein PRO1312.

XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX pharmaceutical; receptor immunoadhesin; gene mapping.

OS Homo sapiens.

PN WO9963088-A2.

PD 09-DEC-1999.

XX 02-JUN-1999; 99WO-US012252.

XX 02-JUN-1998; 98US-0087607P.

XX 02-JUN-1998; 98US-008753P.

XX 03-JUN-1998; 98US-0087827P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088025P.

XX 04-JUN-1998; 98US-0088028P.

XX 04-JUN-1998; 98US-0088029P.

XX 04-JUN-1998; 98US-0088030P.

XX 04-JUN-1998; 98US-0088032P.

XX 04-JUN-1998; 98US-0088326P.

XX 05-JUN-1998; 98US-0088167P.

XX 05-JUN-1998; 98US-0088202P.

XX 05-JUN-1998; 98US-0088212P.

XX 05-JUN-1998; 98US-0088217P.

XX 09-JUN-1998; 98US-0088555P.

XX 10-JUN-1998; 98US-0088722P.

XX 10-JUN-1998; 98US-0088730P.

XX 10-JUN-1998; 98US-0088734P.

XX 10-JUN-1998; 98US-0088738P.

XX 10-JUN-1998; 98US-0088740P.

XX 10-JUN-1998; 98US-0088741P.

XX 10-JUN-1998; 98US-0088742P.

XX 10-JUN-1998; 98US-0088810P.

XX 10-JUN-1998; 98US-0088811P.

XX 10-JUN-1998; 98US-0088824P.

XX 10-JUN-1998; 98US-0088825P.

ABU88626 Human sec
ABO34140 Human PRO
ADA46001 Novel hum
ADA76432 Human PRO
ADA19082 Human PRO
ADA61705 Homo sapi
ADB19490 Novel hum
ADB28031 Human PRO
ADA86510 Novel hum
ADA16074 Human PRO
ADA37898 Human sec
ADA47860 Human PRO
ADA21584 Human sec
ADA10371 Human PRO
AGA67655 Human PRO
ADB30682 Human PRO
ADA85958 Novel hum
ADA17915 Human PRO
ADA97170 Human PRO
ADA79474 Human PRO

26 1102 100.0 212 6 ABUS8626
27 1102 100.0 212 6 ABO34140
28 1102 100.0 212 6 ADA46001
29 1102 100.0 212 6 ADA76432
30 1102 100.0 212 6 ADA19082
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34 1102 100.0 212 6 ADA86510
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38 1102 100.0 212 6 ADA21584
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40 1102 100.0 212 6 AGA67655
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44 1102 100.0 212 6 ADA97170
45 1102 100.0 212 6 ADA79474

PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
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 PR 12-JUN-1998; 98US-0088909P.
 PR 12-JUN-1998; 98US-0089103P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089511P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
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 PR 17-JUN-1998; 98US-0089600P.
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 PR 18-JUN-1998; 98US-0089801P.
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 PR 18-JUN-1998; 98US-0089908P.
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 PR 19-JUN-1998; 98US-0089948P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 22-JUN-1998; 98US-0090252P.
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 PR 23-JUN-1998; 98US-0090349P.
 PR 23-JUN-1998; 98US-0090355P.
 PR 24-JUN-1998; 98US-0090423P.
 PR 24-JUN-1998; 98US-0090431P.
 PR 24-JUN-1998; 98US-0090433P.
 PR 24-JUN-1998; 98US-0090444P.
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 PR 24-JUN-1998; 98US-0090461P.
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 PR 24-JUN-1998; 98US-0090533P.
 PR 24-JUN-1998; 98US-0090538P.
 PR 24-JUN-1998; 98US-0090540P.
 PR 24-JUN-1998; 98US-0090557P.
 PR 25-JUN-1998; 98US-0090676P.
 PR 25-JUN-1998; 98US-0090679P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090690P.
 PR 25-JUN-1998; 98US-0090691P.
 PR 25-JUN-1998; 98US-0090694P.
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 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-0090862P.
 PR 26-JUN-1998; 98US-0090863P.
 PR 01-JUL-1998; 98US-0091358P.
 PR 01-JUL-1998; 98US-0091360P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091486P.
 PR 02-JUL-1998; 98US-0091519P.
 PR 02-JUL-1998; 98US-0091544P.
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 PR 02-JUL-1998; 98US-0091633P.
 PR 02-JUL-1998; 98US-0091646P.
 PR 02-JUL-1998; 98US-0091673P.
 PR 07-JUL-1998; 98US-0091978P.
 PR 07-JUL-1998; 98US-0091982P.
 PR 09-JUL-1998; 98US-0092182P.
 PR 10-JUL-1998; 98US-0092472P.
 PR 20-JUL-1998; 98US-0093339P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 04-AUG-1998; 98US-0095282P.
 PR 04-AUG-1998; 98US-0095285P.
 PR 04-AUG-1998; 98US-0095301P.
 PR 04-AUG-1998; 98US-0095302P.
 PR 04-AUG-1998; 98US-0095318P.
 PR 04-AUG-1998; 98US-0095321P.
 PR 04-AUG-1998; 98US-0095325P.
 PR 10-AUG-1998; 98US-0095916P.

PR 10-AUG-1998; 98US-0095929P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 11-AUG-1998; 98US-0096143P.
 PR 11-AUG-1998; 98US-0096146P.
 PR 12-AUG-1998; 98US-0096329P.
 PR 12-AUG-1998; 98US-0096757P.
 PR 17-AUG-1998; 98US-0096766P.
 PR 17-AUG-1998; 98US-0096768P.
 PR 17-AUG-1998; 98US-0096773P.
 PR 17-AUG-1998; 98US-0096791P.
 PR 17-AUG-1998; 98US-0096867P.
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 PR 17-AUG-1998; 98US-0096894P.
 PR 17-AUG-1998; 98US-0096895P.
 PR 17-AUG-1998; 98US-0096897P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096950P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 18-AUG-1998; 98US-0096960P.
 PR 18-AUG-1998; 98US-0097022P.
 PR 19-AUG-1998; 98US-0097141P.
 PR 20-AUG-1998; 98US-0097218P.
 PR 24-AUG-1998; 98US-0097661P.
 PR 26-AUG-1998; 98US-0097951P.
 PR 26-AUG-1998; 98US-0097952P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097955P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097974P.
 PR 26-AUG-1998; 98US-0097978P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 26-AUG-1998; 98US-0097986P.
 PR 26-AUG-1998; 98US-0098014P.
 PR 31-AUG-1998; 98US-0098525P.
 PR 16-SEP-1998; 98US-0100634P.
 PR 12-JAN-1999; 99US-0115565P.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX WPI; 2000-072883/06.
 DR N-PSDE; AAZ65097.
 XX
 PT Membrane-bound proteins and related nucleotide sequences.
 XX
 PS Claim 12; Fig 278; 822pp; English.

CC The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques

XX Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 3; Length 212;
 Best Local Similarity 100.0%; Pred. No. 5,8e-114;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLMLLPFLVTAIRAEICQPGAEAFKVRISIRIALGDKAYAWDTNTEYLFKAWAFSMRK 60
 |||||
 Db 1 MLMLLPFLVTAIRAEICQPGAEAFKVRISIRIALGDKAYAWDTNTEYLFKAWAFSMRK 60

QY 61 VFNREATEISHVLLCNVTQVSFWFVTPDSKXHTLPAVEVQSAIDMKNKRNINNAFLND 120
 DB 61 VFNREATEISHVLLCNVTQVSFWFVTPDSKXHTLPAVEVQSAIDMKNKRNINNAFLND 120
 QY 121 QTLFLKIPSTLAPPDPSVPIIIFGVIFCIIVAIALLISGIWQRRKKNKPSSEVD 180
 DB 121 QTLFLKIPSTLAPPDPSVPIIIFGVIFCIIVAIALLISGIWQRRKKNKPSSEVD 180
 QY 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212
 DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212

RESULT 2
 AAB33447
 ID AAB33447 standard; protein; 212 AA.
 AC AAB33447;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO1312 protein UNQ678 SEQ ID NO:161.
 XX
 XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 XX dermatological; antiarthritic; antirheumatic; immunosuppressive;
 XX haemostatic; antithyroid; antidiabetic; neutrotropic; neuroprotective;
 XX antianemic; hepatotropic; virucide; antipsoiatic; anti allergic;
 XX antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 XX osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 XX idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 XX systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 XX autoimmune thrombocytopaenia; immune-mediated renal disease;
 XX demyelinating disease; hepatobiliary disease; Whipple's disease;
 XX inflammatory bowel disease; gluten-sensitive enteropathy;
 XX autoimmune disease; immune-mediated skin disease; allergic disease;
 XX immunological disease; transplantation associated disease;
 XX graft rejection; graft-versus-host-disease.
 XX
 OS Homo sapiens.
 XX
 XX WC2000053758-A2.
 XX
 XX 14-SEP-2000.
 PD
 XX 02-MAR-2000; 2000WO-US005841.
 XX
 XX 08-MAR-1999; 99WO-US005028.
 XX 10-MAR-1999; 99US-0123618P.
 XX 12-MAR-1999; 99US-0123957P.
 XX 23-MAR-1999; 99US-0125775P.
 XX 12-APR-1999; 99US-0128849P.
 XX 20-APR-1999; 99WO-US0008615.
 XX 28-APR-1999; 99US-0131445P.
 XX 04-MAY-1999; 99US-0132371P.
 XX 14-MAY-1999; 99US-0134287P.
 XX 02-JUN-1999; 99WO-US012252.
 XX 23-JUN-1999; 99US-0141037P.
 XX 20-JUL-1999; 99US-0144758P.
 XX 26-JUL-1999; 99US-0145698P.
 XX 28-JUL-1999; 99US-0146222P.
 XX 01-SEP-1999; 99WO-US020111.
 XX 08-SEP-1999; 99WO-US020594.
 XX 13-SEP-1999; 99WO-US020944.
 XX 15-SEP-1999; 99WO-US021090.
 XX 15-SEP-1999; 99WO-US021547.
 XX 05-OCT-1999; 99WO-US023089.
 XX 29-NOV-1999; 99WO-US028214.
 XX 30-NOV-1999; 99WO-US028313.
 XX 30-NOV-1999; 99WO-US028409.
 XX 01-DEC-1999; 99WO-US028501.
 XX 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX
 DR WPI; 2000-572271/53.
 DR N-PSDB; AAC58612.
 XX
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
 XX
 PS Claim 33; Fig 68; 309pp; English.
 XX
 CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central and
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
 CC or immune-mediated skin diseases, allergic diseases, immunological
 CC diseases of the lung, and transplantation associated diseases including
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
 CC represent PCR primers and hybridisation probes used in the isolation of
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
 CC represent human PRO polynucleotide and protein sequences given in the
 CC exemplification of the present invention
 XX
 XX Sequence 212 AA;
 SQ
 Query Match 100.0%; Score 1102; DB 3; Length 212;
 Best Local Similarity 100.0%; Pred. NO. 5.8e-114; Indels 0; Gaps 0;
 Matches 212; Conservative 0; Mismatches 0;
 QY 1 MLWLLPFLVTAIHAEICQFGAENAFKVRLSIRTLGDKAYAWDTNEEYLFKAMVAFSMRK 60
 DB 1 MLWLLPFLVTAIHAEICQFGAENAFKVRLSIRTLGDKAYAWDTNEEYLFKAMVAFSMRK 60
 QY 61 VFNREATEISHVLLCNVTQVSFWFVTPDSKXHTLPAVEVQSAIDMKNKRNINNAFLND 120
 DB 61 VFNREATEISHVLLCNVTQVSFWFVTPDSKXHTLPAVEVQSAIDMKNKRNINNAFLND 120
 QY 121 QTLFLKIPSTLAPPDPSVPIIIFGVIFCIIVAIALLISGIWQRRKKNKPSSEVD 180
 DB 121 QTLFLKIPSTLAPPDPSVPIIIFGVIFCIIVAIALLISGIWQRRKKNKPSSEVD 180
 QY 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212
 DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212

AA24430
ID AAB24430 standard; protein; 212 AA.
XX AC AAB24430;
XX DT 07-NOV-2000 (first entry)
XX DE Human PRO1312 protein sequence SEQ ID NO:214.
XX KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
XX KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
XX KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
XX KW cytotactic; gene therapy; vaccine.
XX OS Homo sapiens.
XX PN WO200032221-A2.
XX PD 08-JUN-2000.
XX PF 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1998; 98WO-US025108.
XX PR 16-DEC-1998; 98US-0112850P.
XX PR 12-JAN-1999; 99US-0115554P.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 12-MAR-1999; 99US-0123957P.
XX PR 28-APR-1999; 99US-0131445P.
XX PR 14-MAY-1999; 99US-0134287P.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 26-JUL-1999; 99US-0144758P.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 08-SEP-1999; 99WO-US020594.
XX PR 13-SEP-1999; 99WO-US020944.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 15-SEP-1999; 99WO-US021547.
XX PR 05-OCT-1999; 99WO-US023089.
XX PR 29-OCT-1999; 99US-0162506P.
XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX WPI; 2000-412154/35.
XX N-PSDB; AAB77680.
XX PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
XX PT and treating diagnosing a cardiovascular, endothelial or angiogenic
XX PT disorders in mammals.
XX PS Claim 72; Fig 86; 315pp; English.
XX CC The present invention describes nucleic acids encoding PRO polypeptides
XX CC useful for preventing, diagnosing and treating diagnosing a
XX CC cardiovascular, endothelial or angiogenic disorder in mammals by
XX CC modulating cell proliferation, angiogenesis and cardiovascularisation,
XX CC and for identifying agonists and antagonists of these processes. The
XX CC nucleic acids and the proteins they encode may be used in the prevention,
XX CC treatment and diagnosis of diseases associated with inappropriate PRO
XX CC expression such as cardiovascular, endothelial or angiogenic disorders in
XX CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
XX CC example, the nucleic acids (Ncs) and vectors containing them and the PRO
XX CC polypeptide may be used to treat disorders associated with decreased PRO
XX CC expression. AAB77510 to AAB77721 and AAB24388 to AAB24435 represent
XX CC nucleotide and protein sequences used in the exemplification of the
XX CC present invention
XX CC Sequence 212 AA;
XX SQ

Query Match 100.0%; Score 1102; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114; Indels 0; Gaps 0;
Matches 212; Conservative 0; Mismatches 0;
Qy 1 MLWLLPFLVTAIHAELCQCGAENAFKVRISIRLTALGDKAYADTNEEYLFKAWVAFSMRK 60
Db 1 MLWLLPFLVTAIHAELCQCGAENAFKVRISIRLTALGDKAYADTNEEYLFKAWVAFSMRK 60
Qy 61 VPREATEISHVLICNVTVQVSFWVVDPSKNHTLPAVEVQSAIRNMKNRINNAPFLND 120
Db 61 VPREATEISHVLICNVTVQVSFWVVDPSKNHTLPAVEVQSAIRNMKNRINNAPFLND 120
Qy 121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRKKKEPSEVD 180
Db 121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRKKKEPSEVD 180
Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
Db 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
RESULT 4
AAU12412
ID AAU12412 standard; protein; 212 AA.
XX AC AAU12412;
XX DT 24-OCT-2001 (first entry)
XX DE Human PRO1312 polypeptide sequence.
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
XX KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
XX KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
XX KW A-peptide; factor VIIa; gene therapy.
XX OS Homo sapiens.
XX PN WO200140466-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US032678.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 02-DEC-1999; 99WO-US028564.
XX PR 02-DEC-1999; 99WO-US028565.
XX PR 09-DEC-1999; 99US-0170262P.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030911.
XX PR 30-DEC-1999; 99WO-US031243.
XX PR 30-DEC-1999; 99WO-US031274.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000277.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US000365.
XX PR 18-FEB-2000; 2000WO-US000341.
XX PR 18-FEB-2000; 2000WO-US000342.
XX PR 22-FEB-2000; 2000WO-US000414.
XX PR 24-FEB-2000; 2000WO-US000491.
XX PR 24-FEB-2000; 2000WO-US005004.
XX PR 01-MAR-2000; 2000WO-US005601.
XX PR 02-MAR-2000; 2000WO-US005641.
XX PR 03-MAR-2000; 2000US-0187202P.
XX PR 10-MAR-2000; 2000WO-US006319.
XX PR 15-MAR-2000; 2000WO-US006884.
XX PR 20-MAR-2000; 2000WO-US007377.
XX PR 21-MAR-2000; 2000WO-US007532.
XX PR 30-MAR-2000; 2000WO-US008439.
XX PR 17-MAY-2000; 2000WO-US013705.

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PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2001-408281/43.
XX N-PSDB; AAS21484.
XX
XX Isolated , secretory and transmembrane PRO polypeptide used to detect
XX other PRO polypeptides, link bioactive molecules to cells expressing PRO
XX polypeptides, and detect the presence of mammalian tumors e.g. lung,
XX breast, prostate, cervical.
XX
XX Claim 12; Fig 482; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
XX polypeptides. The PRO polypeptides are useful to detect other PRO
XX polypeptides, to link bioactive molecules to cells expressing PRO
XX polypeptides, to modulate biological activities of cells expressing PRO
XX polypeptides, and to detect the presence of mammalian lung, colon,
XX breast, prostate, rectal, cervical or liver tumours by comparing PRO
XX polypeptide expression in a cell sample to that in a control sample. Some
XX of the 275 sequences are also useful to stimulate the release of tumour
XX necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
XX differentiation of chondrocytes, the proliferation or gene expression in
XX pericyte cells, the release of proteoglycans from cartilage, the
XX proliferation of inner ear utricular supporting cells or of T-
XX lymphocytes, the release of a cytokine from peripheral blood monocytes
XX (PBMCs), or the proliferation of endothelial cells. Some of the PRO
XX polypeptides may modulate glucose or free fatty acid uptake by skeletal
XX muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
XX VIIa. The PRO polypeptides can be used in assays to identify molecules
XX involved in binding interactions. The polynucleotides encoding PRO
XX polypeptides can be used to generate probes, antisense RNA/DNA,
XX transgenic or knock out animals and can be used in gene therapy
XX
XX SQ Sequence 212 AA;
XX
XX Query Match          100.0%; Score 1102; DB 4; Length 212;
XX Best local similarity 100.0%; Pred. No. 5.8e-114;
XX Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MLWLLFLVTAHAEALCPGAEAFKVLRTIRLTALGDKAYAWMDTNEEYLFKAMVAFSMRK 60
XX Db 1 MLWLLFLVTAHAEALCPGAEAFKVLRTIRLTALGDKAYAWMDTNEEYLFKAMVAFSMRK 60
XX
XX Qy 61 VENEAEIEISHLVLCNTQRTQVSFWFVTDPSKNTLPAVEVQSALRNKRNINNAFLND 120
XX Db 61 VENEAEIEISHLVLCNTQRTQVSFWFVTDPSKNTLPAVEVQSALRNKRNINNAFLND 120
XX
XX Qy 121 QTLFELKIPSTLAPPDPSVPVINTIIFGVIFCIIVIAIALILSGIWRKRNKEPSEVD 180
XX Db 121 QTLFELKIPSTLAPPDPSVPVINTIIFGVIFCIIVIAIALILSGIWRKRNKEPSEVD 180
XX
XX Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
XX Db 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
XX
XX RESULT 5
XX AAB65274

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ID AAB65274 standard; protein; 212 AA.
XX
XX AAB65274;
XX
XX 02-APR-2001 (first entry)
XX
XX Human PRO1312 (UNQ678) protein sequence SEQ ID NO:387.
XX
XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
XX cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX
XX Homo sapiens.
XX
XX WO200073454-A1.
XX
XX 07-DEC-2000.
XX
XX 30-MAR-2000; 2000WO-US008439.
XX
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 07-JUL-1999; 99US-0143048P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 17-AUG-1999; 99US-0149396P.
XX 15-SEP-1999; 99WO-US021090.
XX 08-SEP-1999; 99WO-US021547.
XX 18-OCT-1999; 99US-0158663P.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 24-FEB-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006884.
XX 20-MAR-2000; 2000WO-US007377.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX
XX WPI; 2001-032160/04.
XX N-PSDB; AAF44243.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
XX molecules such as toxins, radiolabels or antibodies, to specific cells,
XX to cause targeted cell death.
XX
XX Claim 12; Fig 278; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins can
XX be used for targeted delivery of bioactive molecules, such as toxins,
XX radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX DNA. They may also be used to produce transgenic animals which are used
XX to develop and screen therapeutically useful reagents. The PRO nucleotide
XX and protein sequence can be used for tissue typing and in treating
XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
XX AAF44470 represent PCR primers and hybridisation probes used in the

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CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 212 AA;

Query Match      100.0%; Score 1102; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMLLFFLVTAHAELOCPGAENAFKVLRSRTALGDKAYAWDNEEYLFKAMVAFSNRK 60
   |||||
DB 1 MMLLFFLVTAHAELOCPGAENAFKVLRSRTALGDKAYAWDNEEYLFKAMVAFSNRK 60
   |||||

QY 61 VFNREATEISHVLLCNVTRQVSFWVVTDPKKNHTLPAVEVQSARINNNAPFLND 120
   |||||
DB 61 VFNREATEISHVLLCNVTRQVSFWVVTDPKKNHTLPAVEVQSARINNNAPFLND 120
   |||||

QY 121 QTLPLKIPSTLAPMDFSPVFIWIIIFGVIFCIIVAIALLLSINWRRKKNKEPSEVD 180
   |||||
DB 121 QTLPLKIPSTLAPMDFSPVFIWIIIFGVIFCIIVAIALLLSINWRRKKNKEPSEVD 180
   |||||

QY 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
   |||||
DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
   |||||

RESULT 6
ABUS58089
ID ABUS58089 standard; protein; 212 AA.
AC ABUS58089;
XX
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #21.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
XX
XX US2003027163-A1.
XX
XX
XX 06-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
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PR 12-JUN-1998; 98US-0089105P.
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PR 19-JUN-1998; 98US-0089947P.
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PR 22-JUN-1998; 98US-0090246P.
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PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.

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PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
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PR 11-AUG-1998; 98US-0096143P.
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PR 12-AUG-1998; 98US-0096329P.
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PR 18-AUG-1998; 98US-0097022P.
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PR 20-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
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PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145622P.
PR 28-JUL-1999; 99US-0145622P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028434.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.

PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFFLVTAIHAEICQFGAENAPKVRLSIRLTALGDKAYADTNEEYLFKAMVAFSMRK 60
DB 1 MLWLLFFLVTAIHAEICQFGAENAPKVRLSIRLTALGDKAYADTNEEYLFKAMVAFSMRK 60
QY 61 VFNREATEISHVLLCNVTQVSFWFVVTDPSPKXHTLPAVEVQSARIMNKRNINNAFLND 120
DB 61 VFNREATEISHVLLCNVTQVSFWFVVTDPSPKXHTLPAVEVQSARIMNKRNINNAFLND 120
QY 121 QTLLEPLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRKKKEPSEVD 180
DB 121 QTLLEFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRKKKEPSEVD 180
QY 181 DAEDKCNMTTENGIPSDPLDMKGGILMMP 212
DB 181 DAEDKCNMTTENGIPSDPLDMKGGILMMP 212

RESULT 7
ABU59167
ID ABU59167 standard; protein; 212 AA.
XX AC ABU59167;
XX DT 28-APR-2003 (first entry)
XX DE Novel human secreted or transmembrane protein PRO1312.
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX OS Homo sapiens.
XX PN US2002132252-A1.
XX PD 19-SEP-2002.
XX PF 14-NOV-2001; 2001US-00990442.
XX PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
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PR 24-NOV-1997; 97US-0066770P.
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PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
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PR 02-JUN-1998; 98US-00876039P.
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PR 03-JUN-1998; 98US-00878217P.
PR 04-JUN-1998; 98US-00880212P.
PR 04-JUN-1998; 98US-00880252P.
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PR 17-JUN-1998; 98US-00896532P.
PR 18-JUN-1998; 98US-00898012P.
PR 18-JUN-1998; 98US-00899072P.
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PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 98WO-US005028.
PR 02-JUN-1999; 98WO-US012252.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 30-NOV-1999; 98WO-US028313.
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PR 20-DEC-1999; 98WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski P;
XX Grimaldi JC, Gurney AL, Kljavin LJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX WPI; 2003-247083/24.
XX N-PSDB; ABX80370.
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
XX are therapeutically useful for enhancing immune response and in cancer
XX treatments.
XX Claim 12; Fig 278; 648pp; English.
XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting PRO polypeptides in a sample, in
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and
XX in modulating at least one biological activity of a cell expressing a PRO
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,
XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
XX useful for treating conditions or disorders where angiogenesis would be
XX beneficial, e.g. wound healing and antegenist of this polypeptide are
XX useful for treating cancerous tumors. PRO812 inhibits vascular
XX endothelial growth factor (VEGF) stimulated proliferation of endothelial
XX cells and is thus useful for inhibiting endothelial cell growth in
XX mammals which would be beneficial in inhibiting tumour growth. PRO826,
XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
XX stimulated T-lymphocytes and are therapeutically useful for enhancing
XX immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
XX retinal neurons cells (PRO1132 is also enhances survival/proliferation of
XX rod photoreceptor cells) and therefore are useful for treating retinal
XX disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
XX and PRO1066 induce proliferation of mammalian kidney mesangial cells,
XX and therefore are useful for treating kidney disorders associated with
XX decreased mesangial cell function such as Berger disease or other
XX nephropathies associated with dermatitis, herpeticiformis or Crohn's
XX disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
XX proliferation and/or redifferentiation of chondrocytes in culture and are
XX thus useful for treating sports injuries, and arthritis. This is the
XX amino acid sequence of a novel human PRO protein
XX Sequence 212 AA;
XX
XX Query Match 100.0%; Score 1102; DB 6; Length 212;
XX Best Local Similarity 100.0%; Pred. No. 5.8e-114;
XX Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MLWLLFLVTAIHAELCPGNAENAFKVLSTRTALGDKAYAWDTNNEVLFKAWAFMRK 60
DB 1 MLWLLFLVTAIHAELCPGNAENAFKVLSTRTALGDKAYAWDTNNEVLFKAWAFMRK 60
QY 61 VPNEEATEISHVLLCNVTQVSFWFVTDPSKNTLPAVEVQSARIMNKNINNAFFLND 120
DB 61 VPNEEATEISHVLLCNVTQVSFWFVTDPSKNTLPAVEVQSARIMNKNINNAFFLND 120
QY 121 QTLFLKIPSTLAPPMDPSVPIWIIIFGVPIICIIIVAILLIILSGIWRKRNKEPSSVD 180
DB 121 QTLFLKIPSTLAPPMDPSVPIWIIIFGVPIICIIIVAILLIILSGIWRKRNKEPSSVD 180

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D5 121 QTLFLKIPSTLAPMPDSVPIWIIIFGVIFCIIVAIALLISGIWQRRRNKKEPSEVD 180
QV 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212
D5 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212

RESULT 8
ID ABUS2679
AC ABUS2679 standard; protein; 212 AA.
AC ABUS2679;
DT 26-JUN-2003 (first entry)
DE Human secreted/transmembrane protein PRO1312.
DE Human; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.
OS Homo sapiens.
XX
XX
XX US2003032023-A1.
XX 13-FEB-2003.
XX
XX 14-NOV-2001; 2001US-00990711.
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0022250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0055186P.
XX 13-NOV-1997; 97US-0055311P.
XX 24-NOV-1997; 97US-0056770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088026P.
XX 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.
XX 04-JUN-1998; 98US-0088030P.
XX 04-JUN-1998; 98US-0088033P.
XX 04-JUN-1998; 98US-0088326P.
XX 05-JUN-1998; 98US-0088167P.
XX 05-JUN-1998; 98US-0088202P.
XX 05-JUN-1998; 98US-0088212P.
XX 05-JUN-1998; 98US-0088217P.
XX 09-JUN-1998; 98US-0088655P.
XX 10-JUN-1998; 98US-0088734P.
XX 10-JUN-1998; 98US-0088738P.
XX 10-JUN-1998; 98US-0088742P.
XX 10-JUN-1998; 98US-0088810P.
XX 10-JUN-1998; 98US-0088824P.
XX 10-JUN-1998; 98US-0088826P.
XX 11-JUN-1998; 98US-0088858P.
XX 11-JUN-1998; 98US-0088851P.
XX 11-JUN-1998; 98US-0088876P.
XX 12-JUN-1998; 98US-0089105P.
XX 16-JUN-1998; 98US-0089440P.
XX 16-JUN-1998; 98US-0089512P.
XX 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
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PR 18-JUN-1998; 98US-0089801P.
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PR 18-JUN-1998; 98US-0089908P.
PR 18-JUN-1998; 98US-0089947P.
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PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
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PR 24-JUN-1998; 98US-0090431P.
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PR 24-JUN-1998; 98US-0090444P.
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PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090542P.
PR 24-JUN-1998; 98US-0090557P.
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PR 25-JUN-1998; 98US-0090733P.
PR 25-JUN-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091526P.
PR 02-JUL-1998; 98US-0091628P.
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PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
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PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
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PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.

PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028554.
PR 02-DEC-1999; 99WO-US028556.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030311.
PR 20-DEC-1999; 99WO-US030399.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005941.
PR 10-MAR-2000; 2000WO-US006319.
PR 13-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006866.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882536.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 08-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PR (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX

XX WPI; 2003-341980/32.
XX N-PSDB; ACD24093.
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX Claim 12; Fig 482; 660pp; English.
XX The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell, stimulate the
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX Sequence 212 AA;
SQ

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5, 8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLWLLFFLVTAHAEICQGAENAFKVRISIRLTALGDKAYAWDTNBEYLFKAMVAFSMRK 60
DB 1 MLWLLFFLVTAHAEICQGAENAFKVRISIRLTALGDKAYAWDTNBEYLFKAMVAFSMRK 60
QY 61 VFNREATEISHVLLCNVTQVSFWFVTDPSKNHTLPAVEVOSAIRMKNRINNAPFLND 120
DB 61 VFNREATEISHVLLCNVTQVSFWFVTDPSKNHTLPAVEVOSAIRMKNRINNAPFLND 120
QY 121 QTLEFLKIPSTLAPPMDPSVPIIIFGVIFCIIIVAILLISGIVQRRRKNKPSPEVD 180
DB 121 QTLEFLKIPSTLAPPMDPSVPIIIFGVIFCIIIVAILLISGIVQRRRKNKPSPEVD 180
QY 181 DAEDKCNMTIENGIPSDPLDMKGILMMP 212
DB 181 DAEDKCNMTIENGIPSDPLDMKGILMMP 212

RESULT 10
ABU60598
ID ABU60598 standard; protein; 212 AA.
XX AC ABU60598;
XX 01-MAY-2003 (first entry)
XX Human secreted/transmembrane protein, #157.
XX Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
XX diagnostic; therapeutic; gene therapy.
XX Homo sapiens.
XX US2002160384-A1.
PN

XX PD 31-OCT-2002.
 XX PF 14-NOV-2001; 2001US-0092598.
 XX PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97US-0030006P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065711P.
 PR 24-NOV-1997; 97US-0065770P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088030P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 04-JUN-1998; 98US-0088126P.
 PR 05-JUN-1998; 98US-0088167P.
 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089592P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-SEP-1999; 99WO-US021050.
 PR 30-NOV-1999; 99WO-US021547.
 PR 01-DEC-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 XX PA (GBTH) GENENTECH INC.
 XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski P;
 PI Grimaldi JC, Gurney AL, Kijavini TJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX WI: 2003-288106/28.
 XX N-PSDB; ABX90348.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.

Claim 12; Fig 278; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The sequences presented in AB060478-AB060624 are the PRO polynucleotides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;
 Best Local Similarity 100.0%; Pred. No. 5.8e-114;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLMLFLVTAHAEICQCAENAFKVRISIRLTALGDKAYAMDTNEEYLFKAMVAFSMRK 60
 DB 1 MLMLFLVTAHAEICQCAENAFKVRISIRLTALGDKAYAMDTNEEYLFKAMVAFSMRK 60
 QY 61 VNRTEATISHVLLCMVTORVSFWVTDPSPKHTLPAYEVQSAIPMKNRINNAFLND 120

Db 61 VFNREATEISHYLLCNVTQRVSEFWVTDPSKQHTLPAVEQSAIRMMKNINNAFFLND 120
QY 121 QTLFELKIPSTLAPMDESVPWIIIFGVIFCIITVAIIILSGIWMORRRKNKEPSEVD 180
Db 121 QTLFELKIPSTLAPMDESVPWIIIFGVIFCIITVAIIILSGIWMORRRKNKEPSEVD 180
QY 181 DAEDKCNMITEINGIPSDPLDMKGILMMP 212
Db 181 DAEDKCNMITEINGIPSDPLDMKGILMMP 212
RESULT 11
ABU13980
ID ABU13980 standard; protein; 212 AA.
XX AC ABU13980;
XX XX
DT 26-FEB-2003 (first entry)
XX Human PRO1312 polypeptide.
DE Human; PRO polypeptide; secreted protein; transmembrane protein;
KW Genetic disorder; antibacterial; immunosuppressive.
XX Homo sapiens.
XX OS
XX US2002103125-A1.
XX PD
XX 01-AUG-2002.
XX 20-NOV-2001; 2001US-00989731.
XX 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0055186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0056770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0097106P.
PR 02-JUN-1998; 98US-0087607P.
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PR 03-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
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PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
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PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
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PR 10-JUN-1998; 98US-0088824P.
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PR 11-JUN-1998; 98US-0088858P.
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PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
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PR 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089532P.
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PR 17-JUN-1998; 98US-0089599P.
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PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 02-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US020710.
PR 23-AUG-2000; 2000WO-US020710.
PR 23-AUG-2000; 2000WO-US023522.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021065.
PR 28-AUG-2001; 2001WO-US021735.
XX XX
PA (GETH) GENENTECH LTD.
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI; 2003-102117/09.
DR N-PSDB; ABX64194.
XX XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX Claim 12; Fig 278; 649pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO

CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The polynucleotide sequences
 CC encoding PRO polypeptides are useful as hybridisation probes, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC in the preparation of PRO polypeptides, for generating transgenic animals
 CC or knockout animals, to construct hybridisation probes for mapping the
 CC gene which encodes the PRO polypeptide, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, for chromosome
 CC identification, as chromosome markers, and for generating probes for PCR,
 CC Northern analysis, Southern analysis and Western analysis. ABUI3860-
 CC ABUI4006 represent the human PRO polypeptides of the invention. Note: The
 CC sequence data for this patent was obtained in electronic format directly
 CC from the USPTO web site at seqdata.uspto.gov/psipSIDentry.html
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;
 Best Local Similarity 100.0%; Pred. No. 5.8e-114;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLPLPELVTAHAEALCPGAEAPKVELSIRLTALGKAYAWDTNEEYLPKAWAFNRK 60
 DB 1 MVLPLPELVTAHAEALCPGAEAPKVELSIRLTALGKAYAWDTNEEYLPKAWAFNRK 60

QY 61 VFNREATEISHVLLCNVTQRVSPFWVTPDPSKNHTLPAVEVQSAIRMMKNRINNAPFLND 120
 DB 61 VFNREATEISHVLLCNVTQRVSPFWVTPDPSKNHTLPAVEVQSAIRMMKNRINNAPFLND 120

QY 121 QTLLEKLPSTLAPMPDPSVPIWIIIFGVICIIIVAILLISGIMORRRKKEPEVD 180
 DB 121 QTLLEKLPSTLAPMPDPSVPIWIIIFGVICIIIVAILLISGIMORRRKKEPEVD 180

QY 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212
 DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212

RESULT 12

ID ABU81110 standard; protein; 212 AA.
 AC ABU31110;
 XX
 XX
 DT 23-JUN-2003 (first entry)
 XX
 XX Human PRO polypeptide #241.
 XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
 KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
 KW sports injury; osteoarthritis; hyper-insulinemia; hypo-insulinaemia;
 KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
 KW antidiabetic; anorectic; vulnary; antiarthritic; osteopathic;
 KW antirheumatic; auditory; cerebroprotective; angiogenic.
 XX Homo sapiens.
 OS
 XX
 XX US2003004311-A1.
 XX
 XX
 PD 02-JAN-2003.
 XX
 XX
 PF 19-DEC-2001; 2001US-00028072.
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 XX 18-JUN-1997; 97US-0049911P.
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.

PR 19-SEP-1997; 97US-0059352P.
 PR 19-SEP-1997; 97US-0059388P.
 PR 24-SEP-1997; 97US-0059836P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 17-OCT-1997; 97US-0063755P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063561P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 11-DEC-1997; 97US-0069212P.
 PR 11-DEC-1997; 97US-0069378P.
 PR 11-DEC-1997; 97US-0069314P.
 PR 16-DEC-1997; 97US-0069594P.
 PR 23-JAN-1998; 98US-0072320P.
 PR 04-FEB-1998; 98US-0073612P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 31-MAR-1998; 98US-0079728P.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 23-OCT-1998; 98WO-US022991.
 PR 23-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 13-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028552.
PR 02-DEC-1999; 99WO-US028553.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005501.
PR 02-MAR-2000; 2000WO-US005746.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CX, Wood WI, Zhang Z;
XX
XX WPI; 2003-352836/33.
XX N-PSDB; ACA67234.
XX
XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
XX Claim 12; Fig 482; 643pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. AB0870-AB081144 represent the human PRO
CC polypeptides of the invention. Note: the sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDiEntry.html
XX
XX Sequence 212 AA;
XX
XX Query Match 100.0%; Score 1102; DB 6; Length 212;
XX Best Local Similarity 100.0%; Pred. NC. 5.8e-114;
XX Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 MLWLLFPLVTAIAELCQCAENAFKVRISIRALGDKAYADTNEYLFKAWAFSMRK 60
XX 1 MLWLLFPLVTAIAELCQCAENAFKVRISIRALGDKAYADTNEYLFKAWAFSMRK 60
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XX 61 VPNREATEISHVLLCNVQVSFWFVVTDPKXHTLPAVEVQSAIRMKNRINNAFFLND 120
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XX 181 DAEDKCNMTIENGIPSDLDKMGGLMMP 212
XX 181 DAEDKCNMTIENGIPSDLDKMGGLMMP 212

RESULT 13
ABU72565
ID ABU72565 standard; protein; 212 AA.
XX
XX AC ABU72565;
XX
XX DT 17-JUN-2003 (first entry)
XX
XX DE Novel human secreted and transmembrane protein PRO1312.
XX
XX KW Human, secreted and transmembrane protein; cytostatic; anti-HIV;
XX KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
XX KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
XX KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
XX KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
XX KW drug screening.
XX
XX OS Homo sapiens.
XX
XX US2003003531-A1.
XX
XX PD 02-JAN-2003.
XX
XX PF 19-NOV-2001; 2001US-00989734.
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XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0068770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088026P.
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XX 17-JUN-1998; 98US-0089600P.
XX 17-JUN-1998; 98US-0089653P.
XX 18-JUN-1998; 98US-0089801P.

PR 20-APR-1999; 99WO-US0008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US013252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 03-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030939.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 05-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-0079498.
PR 01-MAR-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00803689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00860208.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.

PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 08-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff B, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-332040/31.
DR N-PSDB; ACA03843.
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX Claim 12; Fig 482; 660pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipdbEntry.html
XX SQ Sequence 212 AA;
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114; Mismatches 0; Gaps 0;
Matches 212; Conservative 0; Indels 0; Gaps 0;
QY 1 MLWLLFFLVTAHAEELCQFGAENAPKVLRSIRLTALGDYAWDTNRYLFXAMVAFSMRK 60
DB 1 MLWLLFFLVTAHAEELCQFGAENAPKVLRSIRLTALGDYAWDTNRYLFXAMVAFSMRK 60
QY 61 VFNREATEISHVLLCNVTQVSFVFTDPSKNHTLPAVEQSALRMKNRINNAFFLND 120
DB 61 VFNREATEISHVLLCNVTQVSFVFTDPSKNHTLPAVEQSALRMKNRINNAFFLND 120
QY 121 QTFLEFKIPSTLAPPMPDSVPWIIIFGVIFCIITVAIIALLISGIIWQRRKNKEPSVD 180
DB 121 QTFLEFKIPSTLAPPMPDSVPWIIIFGVIFCIITVAIIALLISGIIWQRRKNKEPSVD 180
QY 181 DAEDKCNMTIENGIPSDPLDMKGILMPS 212
DB 181 DAEDKCNMTIENGIPSDPLDMKGILMPS 212
RESULT 15
ABU59891
ID ABU59891 standard; protein; 212 AA.
XX ABU59891;
XX AC ABU59891;
XX XX
DT 13-MAY-2003 (first entry)

XX DE Novel secreted and transmembrane protein PRO1312.
 XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 XX KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
 XX OS Homo sapiens.
 XX XX US2003017563-A1.
 XX PD 23-JAN-2003.
 XX XX
 XX PF 07-MAY-2002; 2002US-00140808.
 XX XX
 XX 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US020731.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 01-MAR-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001WO-US017800.
 PR 14-JUN-2001; 2001US-00874503.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen MS, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI: 2003-148238/14.
 DR N-PSDB, ABX89381.
 XX
 PT Two hundred and seventy five nucleic acids encoding PRO polypeptides,
 PT useful for treating pericyte-associated tumors, diabetes and various bone
 PT and/or cartilage disorders, e.g. arthritis.
 XX
 XX Claim 12; Fig 482; 659pp; English.
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO826, PRO1068 or PRO515, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus

CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or Crohn's
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 5.8e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLWLLFVLVTAIHAELOCPGAENAFKVLRSIRLTALGDKAYAWDTNEEYLFKAWVAFSMRK 60
QY 61 VPKREATEISHVLLCNVTQKVSFWFVVDPSKNHTLPAVEVQSARIMNKNRINNAPFLND 120
DB 61 VENREATEISHVLLCNVTQKVSFWFVVDPSKNHTLPAVEVQSARIMNKNRINNAPFLND 120
QY 121 QTLFLKIPSTLAPMDPSVPIIIFGVIFCIIVATALLILSGIMORREKNKEPSEVD 180
DB 121 QTLFLKIPSTLAPMDPSVPIIIFGVIFCIIVATALLILSGIMORREKNKEPSEVD 180
QY 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212
DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212

Search completed: April 1, 2004, 16:26:25
Job time : 63 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

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Run on: April 1, 2004, 16:25:14 ; Search time 22 Seconds
        (without alignments)
        497.487 Million cell updates/sec
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Title: US-09-997-641-387
Perfect score: 1102
Sequence: 1 MLMLFFVNTAIHAELCPG.....ENGIPSDPLDMKGILMMS 212

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2/6/ptodata/2/iaa/6B COMB. pep:*
5: /cgn2/6/ptodata/2/iaa/POTUS COMB. pep:*
6: /cgn2/6/ptodata/2/iaa/backfiles pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	376	34.1	805	3	US-08-988-299-2	Sequence 2, Appli
2	376	34.1	805	4	US-10-158-847-142	Sequence 142, App
3	376	34.1	805	4	US-09-407-427-2	Sequence 2, Appli
4	359	32.6	711	4	US-10-158-847-138	Sequence 138, App
5	289	26.2	681	4	US-10-158-847-140	Sequence 140, App
6	90	8.2	799	1	US-08-188-228-42	Sequence 42, Appl
7	90	8.2	799	1	US-08-338-638-42	Sequence 42, Appl
8	89.5	8.1	793	1	US-08-188-228-54	Sequence 54, Appl
9	89.5	8.1	793	1	US-08-332-643-48	Sequence 48, Appl
10	89.5	8.1	793	1	US-08-332-638-54	Sequence 54, Appl
11	88	8.0	363	1	US-07-946-497-7	Sequence 7, Appli
12	88	8.0	363	1	US-08-483-322-7	Sequence 7, Appli
13	88	8.0	363	2	US-08-478-882-7	Sequence 7, Appli
14	86	7.8	503	1	US-07-946-497-2	Sequence 2, Appli
15	86	7.8	503	1	US-08-483-322-2	Sequence 2, Appli
16	86	7.8	503	2	US-08-478-880-3	Sequence 2, Appli
17	84.5	7.7	339	2	US-08-892-880-3	Sequence 3, Appli
18	83.5	7.6	1337	3	US-08-854-585-2	Sequence 2, Appli
19	83.5	7.6	1337	4	US-09-447-0533-2	Sequence 2, Appli
20	83.5	7.6	1337	5	PCR-US95-05512-2	Sequence 2, Appli
21	82.5	7.5	429	4	US-09-134-000C-5948	Sequence 5948, Ap
22	78.5	7.1	438	4	US-09-404-879A-390	Sequence 390, App
23	78.5	7.1	833	4	US-09-404-879A-389	Sequence 389, App
24	78.5	7.1	914	4	US-09-404-879A-312	Sequence 312, App
25	78.5	7.1	914	4	US-09-338-933-312	Sequence 312, App
26	75.5	6.9	944	4	US-09-107-532A-4864	Sequence 4864, Ap
27	75.5	6.9	2035	2	US-08-479-537A-2	Sequence 2, Appli

Query Match	34.1%	Score 376;	DB 3;	Length 805;
Best Local Similarity	47.9%	Pred. No. 1.4e-34;		
Matches	79;	Conservative 32;	Mismatches 48;	Indels 6; Gaps 3;

19	PGAEAFKVRUSIR	TALGDKAY	MDTNEYI	FLKAMVAFSMR	-----KVPNREAT	-ELSHVL	73
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612	PYAQDSIKVRS	LSLKSADKAY	ENDWENMY	LFSSVAYAMQY	FLUKVKNQML	FGSEQVR	671
	:	:	:	:	:	:	
74	LCNVTQVR	SFVFWVTDPSK	-NHTLFAVEQ	QSAIRNKKR	INNAPFLNDQ	TLEFLKIPSTL	132

ALIGNMENTS

RESULT 1
 US-08-989-299-2
 ; Sequence 2, Application US/08989299
 ; Patent No. 6194556
 ; GENERAL INFORMATION:
 ; APPLICANT: Acton, Susan L.
 ; APPLICANT: Robinson, Keith E.
 ; TITLE OP INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
 ; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109-2170
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/989,299
 ; FILING DATE: 11-Dec-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Arnold E., Beth
 ; REGISTRATION NUMBER: 35,430
 ; REFERENCE/DOCKET NUMBER: MIA-025.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 805 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; 8-04-989-299-2

Query Match	34.1%	Score 376;	DB 3;	Length 805;
Best Local Similarity	47.9%	Pred. No. 1.4e-34;		
Matches	79;	Conservative 32;	Mismatches 48;	Indels 6; Gaps 3;

19	PGAEAFKVRUSIR	TALGDKAY	MDTNEYI	FLKAMVAFSMR	-----KVPNREAT	-ELSHVL	73
	:	:	:	:	:	:	
612	PYAQDSIKVRS	LSLKSADKAY	ENDWENMY	LFSSVAYAMQY	FLUKVKNQML	FGSEQVR	671
	:	:	:	:	:	:	
74	LCNVTQVR	SFVFWVTDPSK	-NHTLFAVEQ	QSAIRNKKR	INNAPFLNDQ	TLEFLKIPSTL	132

Db 672 VANLKPRIISFNFTAPKNVSDIIPRTVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 731
QY 133 APPMDPSVPIIIFGVIFCIIVAIALLILSGIWMQRKKKEPS 177
Db 732 GPPNQPPVSIWLVFVGMVGVIVGIVILIFTGIRDRKKKAKARS 776

RESULT 2

US-10-158-847-142
; Sequence 142, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 142
; LENGTH: 805
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-142

Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAEAFKVLRSIRLTALGDKAYAWDTNEEYLFKAMVAFSMR---KVPNREAT-EISHVL 73
Db 612 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMQYFLKVKQNMILFGEEDVR 671
QY 74 LCNVTQVRSFWFVVDPSK-NHTLPAYEVQSAIRMNKRNINNAFFLNDOTLEFLKIPSTL 132
Db 672 VANLKPRIISFNFTAPKNVSDIIPRTVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 731
QY 133 APPMDPSVPIIIFGVIFCIIVAIALLILSGIWMQRKKKEPS 177
Db 732 GPPNQPPVSIWLVFVGMVGVIVGIVILIFTGIRDRKKKAKARS 776

RESULT 3

US-09-407-427-2
; Sequence 2, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
; FILE REFERENCE: MNT-132CP2
; CURRENT APPLICATION NUMBER: US/09/407,427
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 2
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-407-427-2

Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

QY 19 PGAEAFKVLRSIRLTALGDKAYAWDTNEEYLFKAMVAFSMR---KVPNREAT-EISHVL 73
Db 612 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMQYFLKVKQNMILFGEEDVR 671
QY 74 LCNVTQVRSFWFVVDPSK-NHTLPAYEVQSAIRMNKRNINNAFFLNDOTLEFLKIPSTL 132
Db 672 VANLKPRIISFNFTAPKNVSDIIPRTVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 731
QY 133 APPMDPSVPIIIFGVIFCIIVAIALLILSGIWMQRKKKEPS 177
Db 732 GPPNQPPVSIWLVFVGMVGVIVGIVILIFTGIRDRKKKAKARS 776

RESULT 4

US-10-158-847-138
; Sequence 138, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 138
; LENGTH: 711
; TYPE: PRT
; ORGANISM: homo sapiens
; NAME/KEY: MISC FEATURE
; LOCATION: (219)..(219)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (499)..(499)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-138

Query Match 32.6%; Score 359; DB 4; Length 711;

Best Local Similarity 47.2%; Pred. No. 1.1e-32;
Matches 75; Conservative 32; Mismatches 46; Indels 6; Gaps 3;

QY 19 PGAEAFKVLRSIRLTALGDKAYAWDTNEEYLFKAMVAFSMR---KVPNREAT-EISHVL 73
Db 551 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMQYFLKVKQNMILFGEEDVR 610
QY 74 LCNVTQVRSFWFVVDPSK-NHTLPAYEVQSAIRMNKRNINNAFFLNDOTLEFLKIPSTL 132
Db 611 VANLKPRIISFNFTAPKNVSDIIPRTVEKAIKMSRSRINDAFRLNDSLEFLGIQPTL 670
QY 133 APPMDPSVPIIIFGVIFCIIVAIALLILSGIWMQRKKKEPS 171
Db 671 GPPNQPPVSIWLVFVGMVGVIVGIVILIFTGIRDRKK 709

RESULT 5

US-10-158-847-140
; Sequence 140, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-188-228-42

Query Match      8.3%; Score 90; DB 1; Length 799;
Best Local Similarity 21.4%; Pred. No. 0.2;
Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11

QY      13 HAEICCPGAKNAKFKVRLSIRLTALGDKAYAWDT-----NEEYLFKAWAFSMRKYPN 63
DB      432 HTDLERQFNADDGKITATPLDRLSVWNIISIAIEIRNHSSQISVPVAIKVLVDV-N 490
QY      64 REATEIGS---HVLIC-----NYTQRVSFWVFVTDPKSNH-----TLPAVEVQSASIRMNK 109
DB      491 DNAEPFASEYEALFCENGKRGQVIQTWSA-MDKDDPQNGHPFLYSILLPEMVANNPNFTKK 549
QY      110 NRINNAEFL-----NDQILEPLKIPSTLA----PPMDPSVPIWIILPG-----148
DB      550 NEDNSLSILAKHGFRNQKEQVLLPEIVISDGNPPLSGTSTLTITRVCGCSNDGVVVQSCN 609
QY      149 -----VFCCIIVAAILLGSIGWRRRKNKEPSEVDAEDKCNMIT 191
DB      610 VEAYVLPGLSMGALLACIILLLVIVLP--VTLRHKN-EPLIKDDEVDRENIIR 666
QY      192 IEN 194
DB      667 YDD 669

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RESULT 7
US-08-332-638-42
Sequence 42, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 799 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-332-638-42

Query Match 8.2%; Score 90; DB 1; Length 799;
 Best Local Similarity 21.4%; Pred. No. 0.2;
 Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;

QY 13 HAEIQCPGAENAFKRLSIRIALGDKAYAWDT-----NEEYLFKAMVAFSMRKVPN 63
 DB 432 HTDLERQFNINADGGKITLATPLDRELSDWHNISIATEIRNHSQISRPVPAIKVLDV-N 490
 QY 64 REATEIS---HVLIC-----NVTQVSFWFVTDPSKNH-----TLPAVEVQSAIRMNK 109
 DB 491 DNAPEFASYEAFLENGKPGQVIQTVSA-MDKDDPKNGHFFLYSLLEPMVNNPFTIKK 549
 QY 110 NRINNAFL-----NDQTLFLKIPSTLA-----PPMDPSVPPIWIIIFG----- 148
 DB 550 NEDNSLSILAKHNGFNQKQEVYLLPIVISGNNPPLSSTLTIRVCGCSNDGVQSCN 609
 QY 149 -----VFCHIIIVAIALLISGIWQRNRKNKEPSEVDDAEDKCNMIT 191
 DB 610 VEAYVLPGLSGMALIAILACIILLVIVVLF--VTLRRHKN-EPLIKDKDEDVRENIIR 666
 QY 192 IEN 194
 DB 667 YDD 669

RESULT 8

US-08-188-228-54
 Sequence 54, Application US/08188228
 Patent No. 5597725

GENERAL INFORMATION:
 APPLICANT: Suzuki, Shintaro
 TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Borun
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/188.228
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/049,460
 FILING DATE: 19 APR 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,643
 FILING DATE: 17 APR 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5597725and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31340
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448

TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 793 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-188-228-54

Query Match 8.1%; Score 89.5; DB 1; Length 793;
 Best Local Similarity 20.6%; Pred. No. 0.22;
 Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

QY 13 HAEIQCPGAENAFKRLSIRIALGDKAYAWDT-----NEEYLFKAMVAFSMRKVPN 63
 DB 425 HTDLERQFNINADGGKITLATPLDRELSDWHNISIATEIRNHSQISRPVPAIKVLDV-N 483
 QY 64 REATEIS---HVLIC-----NVTQVSFWFVTDPSKNH-----TLPAVEVQSAIRMNK 109
 DB 484 DNAPEFASYEAFLENGKPGQVIQTVSA-MDKDDPKNGHFFLYSLLEPMVNNPFTIKK 542
 QY 110 NRINNAFL-----NDQTLFLKIPSTLA-----PPMDPSVPPIWIIIFG----- 148
 DB 543 NEDNSLSILAKHNGFNQKQEVYLLPIVISGNNPPLSSTLTIRVCGCSNDGVQSCN 602
 QY 149 -----VFCHIIIVAIALLISGIWQRNRKNKEPSEVDDAEDKCNMIT 191
 DB 603 VEAYVLPGLSGMALIAILACIILLVIVVLF--VTLRRHKN-EPLIKDKDEDVRENIIR 660
 QY 192 IEN 194
 DB 661 YDD 663

RESULT 9

US-08-332-643-48
 Sequence 48, Application US/08332643
 Patent No. 5639634

GENERAL INFORMATION:
 APPLICANT: Suzuki, Shintaro
 TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bicknell
 STREET: Two First National Plaza, 20 South Clark
 STREET: Street
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/332,643
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/872,643
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5639634and, Greta B.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/30795
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 346-5750
 TELEFAX: (312) 984-9740
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 793 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-643-48

Query Match      8.1%; Score 89.5; DB 1; Length 793;
Best Local Similarity 20.6%; Pred. No. 0.22;
Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

Qy 13 HAEICQGAENAFKVLRSITATLGDKAYAWDT-----NVEYLKAMVAFSMRKVPN 63
Db 425 HTDLERQFNINADGKITLATPLDRELSVNMHTIATIRNHSQISRVPVAKVLDV-N 483
Qy 64 REATEIS---HVLIC-----NVTQVSFWFVVTDPKSH-----TLPVAVESQAIRMNK 109
Db 484 DNAPEPASEVEAFLENGKPGQVLOTUSA-MDKDDPKNGHYFLYSLPWNPNFTIKK 542
Qy 110 NRINNAFFL-----NDQTLFLKIPSTLA-----PPMDPSVPIWIIIFG-----148
Db 543 NEONSLSILAKHNGFNKQEVYLLPIIISDGNPPLSSTLTIRVCGCSNDGVVQSCN 602
Qy 149 -----VIFCIIVAIALLISGIWRRRKNKEPSEVDDAEKCNMIT 191
Db 603 VEAYVLPGLSMGALIAILACIILLVIVLFP--VTLRRHQNEPLIKDDVDRENIIR 660
Qy 192 IEN 194
Db 661 YDD 663

RESULT 10
US-08-332-638-54
; Sequence 54, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; Zip: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-638-54

Query Match      8.1%; Score 89.5; DB 1; Length 793;
Best Local Similarity 20.6%; Pred. No. 0.22;
Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

Qy 13 HAEICQGAENAFKVLRSITATLGDKAYAWDT-----NVEYLKAMVAFSMRKVPN 63
Db 425 HTDLERQFNINADGKITLATPLDRELSVNMHTIATIRNHSQISRVPVAKVLDV-N 483
Qy 64 REATEIS---HVLIC-----NVTQVSFWFVVTDPKSH-----TLPVAVESQAIRMNK 109
Db 484 DNAPEPASEVEAFLENGKPGQVLOTUSA-MDKDDPKNGHYFLYSLPWNPNFTIKK 542
Qy 110 NRINNAFFL-----NDQTLFLKIPSTLA-----PPMDPSVPIWIIIFG-----148
Db 543 NEONSLSILAKHNGFNKQEVYLLPIIISDGNPPLSSTLTIRVCGCSNDGVVQSCN 602
Qy 149 -----VIFCIIVAIALLISGIWRRRKNKEPSEVDDAEKCNMIT 191
Db 603 VEAYVLPGLSMGALIAILACIILLVIVLFP--VTLRRHQNEPLIKDDVDRENIIR 660
Qy 192 IEN 194
Db 661 YDD 663

RESULT 11
US-07-946-497-7
; Sequence 7, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; ADDRESSEE: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; STREET: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; Zip: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mCD44
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US-07-946-497-7

Query Match 8.0%; Score 88; DB 1; Length 363;
Best Local Similarity 21.6%; Pred. No. 0.11;
Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPPMDPSVPIIIFGVIFCIIVAIALLILSGIWQRRR-----PLDMKGGI 171
Db 256 VTTTSGPMRRPQIPFWLII---LASLLALAILAVCIANRRRCGQKKLVINGNGTV 312

QY 172 KNKEPSEVDDAEDKCNMTIENGIPSD-----PLDMKGGI 207
Db 313 EDRKPSSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLQSDVMKIGV 363

RESULT 12
US-08-483-322-7
; Sequence 7, Application US/08483322
; Patent No. 5786178
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,322
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,497
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mCD44
US-08-483-322-7

Query Match 8.0%; Score 88; DB 1; Length 363;
Best Local Similarity 21.6%; Pred. No. 0.11;
Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPPMDPSVPIIIFGVIFCIIVAIALLILSGIWQRRR-----PLDMKGGI 171
Db 256 VTTTSGPMRRPQIPFWLII---LASLLALAILAVCIANRRRCGQKKLVINGNGTV 312

QY 172 KNKEPSEVDDAEDKCNMTIENGIPSD-----PLDMKGGI 207

Db 313 EDRKPSSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLQSDVMKIGV 363

RESULT 13
US-08-478-882-7
; Sequence 7, Application US/08478882
; Patent No. 5885575
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,882
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mCD44
US-08-478-882-7

Query Match 8.0%; Score 88; DB 2; Length 363;
Best Local Similarity 21.6%; Pred. No. 0.11;
Matches 24; Conservative 23; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPPMDPSVPIIIFGVIFCIIVAIALLILSGIWQRRR-----PLDMKGGI 171
Db 256 VTTTSGPMRRPQIPFWLII---LASLLALAILAVCIANRRRCGQKKLVINGNGTV 312

QY 172 KNKEPSEVDDAEDKCNMTIENGIPSD-----PLDMKGGI 207
Db 313 EDRKPSSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLQSDVMKIGV 363

RESULT 14
US-07-946-497-2
; Sequence 2, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut

```

; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-946-497-2

Query Match 7.8%; Score 86; DB 1; Length 503;
Best Local Similarity 20.7%; Pred. No. 0.29;
Matches 23; Conservative 24; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLLSGIWQRR-----PLDMKGI 207
DB 396 VTTTSGPARRPOIPEWII---LASLALAILAVCIAVNSRRRCGQKKLVNSGNGTV 452

QY 172 KNKEPSEVDDADKCNMTIENGIPSD-----PLDMKGI 207
DB 453 EDRKPSLNGEASKSQEWVHLVKNKEPTETPDQFMTADETRNLSQVDMKIGV 503

RESULT 15
US-08-483-322-2
; Sequence 2, Application US/08483322
; Patent No. 5760178
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-946-497-2

Query Match 7.8%; Score 86; DB 1; Length 503;
Best Local Similarity 20.7%; Pred. No. 0.29;
Matches 23; Conservative 24; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLLSGIWQRR-----PLDMKGI 207
DB 396 VTTTSGPARRPOIPEWII---LASLALAILAVCIAVNSRRRCGQKKLVNSGNGTV 452

QY 172 KNKEPSEVDDADKCNMTIENGIPSD-----PLDMKGI 207
DB 453 EDRKPSLNGEASKSQEWVHLVKNKEPTETPDQFMTADETRNLSQVDMKIGV 503

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; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,322
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,497
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-322-2

Query Match 7.8%; Score 86; DB 1; Length 503;
Best Local Similarity 20.7%; Pred. No. 0.29;
Matches 23; Conservative 24; Mismatches 30; Indels 34; Gaps 3;

QY 128 IPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLLSGIWQRR-----PLDMKGI 207
DB 396 VTTTSGPARRPOIPEWII---LASLALAILAVCIAVNSRRRCGQKKLVNSGNGTV 452

QY 172 KNKEPSEVDDADKCNMTIENGIPSD-----PLDMKGI 207
DB 453 EDRKPSLNGEASKSQEWVHLVKNKEPTETPDQFMTADETRNLSQVDMKIGV 503

Search completed: April 1, 2004, 16:29:00
Job time : 23 secs
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OM protein - protein search, using sw model

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(without alignments)
1356.389 Million cell updates/sec

Title: US-09-997-641-387
Perfect score: 1102
Sequence: 1 MLWLLPFLVTAHRLCQPG.....ENGIPSDPLDMKGGILWMP 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1069545 seqs, 262320428 residues

Total number of hits satisfying chosen parameters: 1069545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1102	100.0	212	9	US-09-989-722-387 Sequence 387, App
2	1102	100.0	212	9	US-09-989-723-387 Sequence 387, App
3	1102	100.0	212	9	US-09-989-279-387 Sequence 387, App
4	1102	100.0	212	9	US-09-989-727-387 Sequence 387, App
5	1102	100.0	212	9	US-09-989-731-387 Sequence 387, App
6	1102	100.0	212	9	US-09-989-732-387 Sequence 387, App
7	1102	100.0	212	9	US-09-991-073-387 Sequence 387, App
8	1102	100.0	212	9	US-09-990-442-387 Sequence 387, App
9	1102	100.0	212	9	US-09-991-163-387 Sequence 387, App
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ALIGNMENTS

RESULT 1
US-09-989-722-387
; Sequence 387, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
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; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989, 723
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIVAIALLISGIWQRKKEPSEVD 180
Db 121 QTLFELKIPSTLAPMDPSVPIWIIIFGVIFCIIVAIALLISGIWQRKKEPSEVD 180

Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
Db 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212

RESULT 3
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; Sequence 387, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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Query Match 100.0%; Score 1102; DB 9; Length 212;
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 DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMWS 212

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 ; Patent No. US20020072497A1
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 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
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 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Fertara, Napoleone
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; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFFLVTAHAEICQPGAEAFKVLISITLGDKAYANDTBEYLFKAWAFSMRK 60
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QY 121 QLEFLKIPSTLAPMDFSVPIWIIIPGVPCIIIVAILLISGIWRRRKNKPSSEVD 180
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US-09-989-731-387
; Sequence 387, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC70
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 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; Patent No. US2002012756A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
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;; PRIOR APPLICATION NUMBER: 60/090535
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3,5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWLLFLVTAHAELCQGAENAFKVRLSIRLTALGDKAYANDTNEEYLFKAWAFSKRK 60
DB 1 MLWLLFLVTAHAELCQGAENAFKVRLSIRLTALGDKAYANDTNEEYLFKAWAFSKRK 60

QY 61 VFNREATEISHVLLCNVTRQVFWFVVTDPKKNHTLPAVEVQSARIMNKNRINNAFFLND 120
DB 61 VFNREATEISHVLLCNVTRQVFWFVVTDPKKNHTLPAVEVQSARIMNKNRINNAFFLND 120

QY 121 QTLFLKIPSTLAPMDPSVPWIIIFGVIFCIIIVAIALLILSGIWRKRRKNKPSPEVD 180
DB 121 QTLFLKIPSTLAPMDPSVPWIIIFGVIFCIIIVAIALLILSGIWRKRRKNKPSPEVD 180

QY 181 DAEDKCNMTTENGIPSPDLNKGKGLMPPS 212
DB 181 DAEDKCNMTTENGIPSPDLNKGKGLMPPS 212

RESULT 8
US-09-990-442-387
; Sequence 387, Application US/09990442

;; Patent No. US20020132252A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David.
;; APPLICANT: Deenoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Geritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas P.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tamas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C8
;; CURRENT APPLICATION NUMBER: US/09/990,442
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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122 PRIOR FILING DATE: 1998-07-07
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124 PRIOR FILING DATE: 1998-07-07
125 PRIOR APPLICATION NUMBER: 60/092182
126 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;

Best Local Similarity 100.0%; Pred. No. 3.5e-113; Mismatches 0; Indels 0; Gaps 0;

Matches 212; Conservative 0;

QY 1 MWLLFFLVTAHAEELCOGAEAFKVLRSIRLTALGDKAYAWDTNNEYLFKAWAFSMRK 60

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DB 121 QTLFELKIPSTLAPPMDPSVPIWIIIFGVIFCIIVAIALLILSGIWRKRRKKEPSEVD 180

QY 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212

DB 181 DAEDKCNMTIENGIPSDPLDMKGGILMPS 212

RESULT 9

US-09-991-163-387
; Sequence 387, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin E.
; APPLICANT: KJ.Javin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 11.02; DB 9; Length 212;
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RESULT 10
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 ; Sequence 387, Application US/09993604
 ; Patent No US20020137075A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730FIC25
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Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 QTLLEKIPSTLAPPMDSVPIMIIIPGVTFCIIIVAIALLIISGIVORRRKNKBPSEVD 180
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Goddard, Audrey
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APPLICANT: Pan, James
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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 ; APPLICANT: Ashkenazi, Avi J.
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Best Local Similarity 100.0%; Pred. No. 3,5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MMLFFFLVTAHAELOCPGAEAFKVLRTALGDKAYADTNEEYLFKAMVAPSRK 60
QY 61 VFNREATEISHLVLLCNVTQVSPFVWVDPDSKNHTLPAVEVQSAIRNMKNRINNAFFLND 120
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QY 121 QTLFLKLPSTLAPMDSPVPIIIFGVIFCIIVAIHALILSGIQRRKXKEPSEVD 180
DB 121 QTLFLKLPSTLAPMDSPVPIIIFGVIFCIIVAIHALILSGIQRRKXKEPSEVD 180
QY 181 DAEDKCNMTITENGIPSDPLDMKGGILMPS 212
DB 181 DAEDKCNMTITENGIPSDPLDMKGGILMPS 212

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US-09-992-598-387
; Sequence 387, Application US/0992598
; Patent No. US20020150384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertschen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
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Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 QTLFLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLISGIWQRNKNKPSSEVD 180
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Qy 181 DAEDKCNMTIENGIPSDPLDMKGGILMMP 212
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RESULT 14

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; Sequence 387, Application US/09989293A
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989, 293A
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLLPFLVTAIHAELCOPGAEAFKVLSTRTALGDKAVANDTNEEYLFKAWAFSMRK 60
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Qy 61 VPNEATEISHLVLCNVTVQVSFWFVVTDPSSKNHTLPAVEVQSAIRMNKRNINNAFLND 120
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US-09-989-735-387
Sequence 387, Application US/09989735
Publication No. US2002019299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Stewart, Timothy A.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
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; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
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; PRIOR APPLICATION NUMBER: 60/090252
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; PRIOR APPLICATION NUMBER: 60/090254
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; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 1102; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 3 5e-113;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLWLLFFLVTAHAELOCQGAENAFKVRSLRTALGDKAYAWDTNEEYLFKAMVAFPSNRK 60
Db 1 MLWLLFFLVTAHAELOCQGAENAFKVRSLRTALGDKAYAWDTNEEYLFKAMVAFPSNRK 60
Qy 61 VPNEATEISHVLLCNVTQVSEFWVTDPKSHHTLPAVEVQSAIRXMKRINNAPFLND 120
Db 61 VPNEATEISHVLLCNVTQVSEFWVTDPKSHHTLPAVEVQSAIRXMKRINNAPFLND 120
Qy 121 QTLFELKIPSTLAPPMPSVPINIIIFGVIFCIIVAIALLIISGIWRRRNKEPSEVD 180
Db 121 QTLFELKIPSTLAPPMPSVPINIIIFGVIFCIIVAIALLIISGIWRRRNKEPSEVD 180
Qy 181 DAEDKCNMTTIENGIPSDPLDMKGGILMMP 212
Db 181 DAEDKCNMTTIENGIPSDPLDMKGGILMMP 212

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Search completed: April 1, 2004, 16:33:44
Job time : 43 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	376	34.1		804	2	T14762	hypothetical prote
2	97.5	8.8		1086	2	T19523	integrin alpha cha
3	94	8.5		704	2	T29996	hypothetical prote
4	92.5	8.4		1153	2	T31080	nitric-oxide synth
5	89.5	8.1		244	2	E86471	unknown protein [i
6	89.5	8.1		793	2	T89992	cadherin 8 - human
7	89.5	8.1		1188	2	T13933	pol polyprotein -
8	89	8.1		1054	2	JC7294	alpaap integrin -
9	88	8.0		363	2	A37009	CD44 homolog membr
10	88	8.0		365	2	A34424	CD44 membrane gly
11	86	7.8		362	2	A35616	T-cell surface gly
12	86	7.8		503	2	B38745	cell adhesion mole
13	85.5	7.8		667	2	T47482	receptor-like prot
14	84.5	7.7		468	2	E81924	probable two-compo
15	84.5	7.7		536	2	JG8022	flagellar basal-bo
16	84.5	7.7		1112	2	T28082	hypothetical prote
17	84	7.6		428	2	I48167	hypothetical prote
18	83.5	7.6		1337	1	I38670	protein-tyrosine-p
19	83	7.5		525	2	B3957	flagellar basal-bo
20	82.5	7.5		1044	2	S16516	integrin alpha-8 c
21	81.5	7.4		252	2	T05813	hypothetical prote
22	81.5	7.4		1048	2	A27421	integrin alpha-5 c
23	81	7.4		1041	2	T11437	integrin alpha cha
24	81	7.4		1135	2	I61186	alpha-7 integrin -
25	80.5	7.3		1034	2	A36108	integrin alpha-v c
26	80	7.3		234	1	Q9B843	membrane antigen g
27	80	7.3		489	2	AF2970	conserved hypothet
28	80	7.3		489	2	D98312	hypothetical prote
29	79.5	7.2		1044	2	T10050	integrin alpha-v c


```

Qy      172 KNKPSVVDADDKCENNIITENGIPSD-----PLDMKGGI 207
          :::|||: | : | ||:
Db      453 EDRKPSBLNGEASKSQEMVLVNKEPTETPDQFMATDTRLNQSVDMKIGV 503
          :::|||: | : | ||:

RESULT 13

T47482
receptor-like protein kinase - Arabidopsis thaliana
N;Alternate names: protein F18n11.180
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: T47482
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseid, M.; Meves, H.W.; Lemcke, K
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24467
A;Accession: T47482
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-667 <Jor>
A;Cross-references: EMBL:AL132953
A;Experimental source: cultivar Columbia; BAC clone F18n11
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C;Genetics:
A:Map position: 3
A:Note: F18N11.180
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 7.8%; Score 85.5; DB 2; Length 667;
Best Local Similarity 21.6%; Pred. No. 6.6;
Matches 37; Conservative 23; Mismatches 64; Indels 47; Gaps 6;

QY 81 VSFVFTVDSKHTLPVAVQSAIR-----MKNKRNINNAFF 117
DB 192 VQWIDYDGLNVTLPAPIEQKPNRLSRDINLSIFQDKMYGFGSGNGRLTSNQYI 251

QY 118 LN-----DOTLEFLKIPSTLAP-----PMDSVPWIIIFGVIFCIIVIAIAL 161
DB 252 LGWSFSKSKPMQSLDLSKLPQAPIPRNEQAPVREKXKHLPLGLV--ILLVIVPLM 309

QY 162 ILSGI-WQRKRNKPEVDVDAE-----DKENMITIENGIPSDFLDMKGG 206
DB 310 VLGGVYVYRKKYAEVKSWEKEGPHRYGKSLYKATNGFVKDALVGGK 360

RESULT 14
881924
probable two-component system sensor kinase (EC 2.7.3.-) NMA0797 [imported] - Neisseria
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: B81924
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81924
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-468 <PAR>
A;Cross-references: GB:AL162754; GB:AL157959; MID:g7379424; PIDN:CAB84080.1; PID:g737951
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A:Gene: NMA0797
C;Keywords: phosphotransferase

Query Match 7.7%; Score 84.5; DB 2; Length 468;
Best Local Similarity 23.7%; Pred. No. 5.4; Indels 41; Gaps 9;
Matches 47; Conservative 29; Mismatches 81; Indels 41; Gaps 9;

QY 21 AENAFKVLRLSIRTA-----GDKAYADTNEEYLFKAMVAFSMRKVPNREATEI 69
DB 34 AENQFNQRTIETTLGSIISAFRAGD-AGAREILTEWK-DSPVSSGVVVIQDDEKDI 91

QY 70 SHVLLCNVTQVSEFWVVDPSKHTLPVAVQSAIRMKRNINNAFFLNDOTLFLKI 126
DB 92 LHRVDSYTIERAKLFAAGHPHSN-----LVHIEYDRGEEYLFPTKDWDXLQAR 141

QY 127 KIPSTLAPPDPSVPIW-----IIIFGVIFCIIVIAIALILSGIWRKRNKPESEVDADKCE 171
DB 142 RLSPSLIPLGLPAPIWHELIIILSVLLMAYILAGNIAPKPIRLNGMDRVANGEL 201

QY 172 KNKPESEVDADKCEKN 189
DB 202 ETRISQVQVDRDRLSHL 219

RESULT 15
JG0022
flagellar basal-body M-ring protein flilP - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 21-Jul-2000
C;Accession: JG0022; A42365; B69624; S14494
R;Zuberi, A.R.; Ying, C.; Bischoff, D.S.; Ordal, G.W.
Gene 101, 23-31, 1991
A;Title: Gene-protein relationships in the flagellar hook-basal body complex of Bacillus

A;Reference number: JG0019; MUID:91285431; PMID:1905667
A;Accession: JG0022
A:Molecule type: DNA
A;Residues: 1-536 <ZUB>
A;Cross-references: GB:M54965
R;Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
J. Bacteriol. 173, 3573-3579, 1991
A;Title: The flaA locus of Bacillus subtilis is part of a large operon coding for flag
A;Reference number: A42365; MUID:91258343; PMID:1828465
A;Accession: A42365
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 355-536 <ALB>
A;Cross-references: GB:M72718; EMBL:X56049; NID:939904; PIDN:CAA39520.1; PID:g3979709
R;Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tanakoshi, A.; Terpstra, P.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.P.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A65580; MUID:98044033; PMID:9384377
A;Accession: B69624
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A;Residues: 1-536 <KUN>
A;Cross-references: GB:299112; GB:AL009126; NID:g2633902; PIDN:CAB13494.1; PID:ell85212
A;Experimental source: strain 168
C;Genetics:
A:Gene: flilP

Query Match 7.7%; Score 84.5; DB 2; Length 536;
Best Local Similarity 19.9%; Pred. No. 6.3;
Matches 39; Conservative 36; Mismatches 68; Indels 53; Gaps 8;

QY 9 VTAIHAELOCPGAENAFKVLRLSIRTAIGDKAYADTNEEYLFKAMVAFSMRKVPNREATE 68
DB 352 VRIHKEI-----AESPKVR-----DLGIQWVEPPDANKTASLSTERQDD 393

QY 69 ISHVLLCNVTQVSEFWVVDPSKHTLPVAVQSAIRMKRNINNAFFLNDOTLFLKI 128
DB 394 IQKIL-STVWTS---LQKDETQNLSDADINNKIVSVQVDFGKVLNDYNTBE--- 444

QY 129 PSTLAPPDPSVPIW-IIIFGVIFCIIVIAIALILSGIWRKRNKPESEVDADKCE 187
DB 445 -----SSGIPLMAYIVGGVLIALLIILMLI-----RKGAQSDSEFEYEYE-- 487

QY 188 NMITIENGIPSDPLDM 203
DB 488 -----VPOBPINL 495

Search completed: April 1, 2004, 16:28:26
Job time : 22 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	92.5	8.4	1153	1	NOS LYMST	O61309 lymnaea sta
2	91	8.3	623	1	SYR_SULTO	O971x1 sulfolobus
3	90	8.2	799	1	CAD8 MOUSE	P97291 mus musculus
4	90	8.2	799	1	CAD8 RAT	O54800 rattus norv
5	89.5	8.1	1025	1	ITAB HUMAN	P53708 homo sapien
6	89	8.1	799	1	CAD8 HUMAN	P52886 homo sapien
7	88	8.0	778	1	CD44 MOUSE	P15379 mus musculus
8	87	7.9	362	1	CD44 CRIGR	P20944 cricetus
9	86	7.8	431	1	CD44 MSAU	Q60522 m cd44 anti
10	86	7.8	503	1	CD44 RAT	P26051 rattus norv
11	84.5	7.7	536	1	FLIF_BACSU	P23447 bacillus su
12	83.5	7.6	1337	1	PTFIP HUMAN	Q12913 homo sapien
13	82.5	7.5	1044	1	ITAB CHICK	P26009 gallus gall
14	82	7.4	1189	1	ITAB HUMAN	Q9ukx5 homo sapien
15	81.5	7.4	363	1	LEUI_PHOLL	P7n128 photorhabdu
16	81.5	7.4	1048	1	ITAV HUMAN	P06756 homo sapien
17	81	7.4	1179	1	ITAV_MOUSE	Q61738 mus musculus
18	80.5	7.3	1034	1	ITAV CHICK	P26008 gallus gall
19	80	7.3	234	1	VGP8_EBV	P03224 Epstein-Bar
20	79.5	7.2	393	1	ILIS_CERA	Q29612 cercopithe
21	79.5	7.2	1044	1	ITAV MOUSE	P43406 mus musculus
22	79	7.2	437	1	YC43_PORPU	P51363 porphyra pu
23	79	7.2	611	1	RBT1_MOUSE	Q9cnc4 mus musculus
24	79	7.2	1033	1	ITAB_MOUSE	Q9qun0 mus musculus
25	79	7.2	2029	1	LAR_DROME	P16621 drosophila
26	78	7.1	343	1	MRGF_RAT	P23749 rattus norv
27	78	7.1	732	1	CADL_CHICK	P33145 gallus gall
28	78	7.1	1022	1	ALAI_ANGAN	Q92030 anguilla an
29	77.5	7.0	351	1	CD44_CANE	Q28284 canis fami
30	77	7.0	322	1	GPT_SULSO	P36000 sulfolobus
31	76.5	6.9	363	1	LEU3_SALTY	P7412 salmonella
32	76.5	6.9	365	1	OPSR_XENLA	Q12948 xenopus lae
33	76.5	6.9	475	1	MUCI_HYLLA	Q29435 hylabates l


```
DR InterPro; IPR001709; FPN_cyt_redtse.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; OxRed_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding_1; 2.
DR Pfam; PF02898; NO_synthase_1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS60001; NOS; 1.
DR Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme; Repeat;
KW Alternative splicing.
FT DOMAIN 427 610
FT METAL 82 82
FT CALMODULIN-BINDING (POTENTIAL).
FT FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 556 587
FT NP_BIND 697 708
FT NP_BIND 836 846
FT NP_BIND 911 929
FT NP_BIND 1089 1104
FT NP_BIND 934 1010
FT [IM]-P-S-C.
FT Missing (in isoform Short).
FT VARSPLIC 276 309
FT /FTIG-VSP 003584.
SQ SEQUENCE 1153 AA; 129085 MW; 101B7D02B66B109 CRC64;

Query Match 8.4%; Score 92.5; DB 1; Length 1153;
Best Local Similarity 21.1%; Pred. No. 1.7;
Matches 64; Conservative 28; Mismatches 135; Gaps 13;

QY 21 AENAFKVLISRTALGKAYADNTNEYLFA-MVAFSMKVPNRE---ATEI----- 69
DB 689 AHNA---TDLKAPGDHVAIPANSPDIVAILVRLDTSGPSDPQVVKTEISPOLG 744
QY 70 ----SHVLLCNVQVSFWFVTDKSKHTEPAVEVQSAIRMYKRI-----NNAFF--- 117
DB 745 DTWRSHLPICTSRTAFSLFDLTTPSQBILOVLATQASSDMRKHQLQASNSAYEK 804
QY 118 ---LNDQTEF-----LKIPSTL-----
DB 805 RLDSLNPILDEPFLSKIPSLALLTQLPLQPRYSSISSQQKNPNEVHATIAVVRPK 864
QY 133 -----AP-----PMDSVPIWIIIFGVIECIIV 156
DB 865 TQDGDGPVHEGVCSWLNARSPITVVPCLRSAPHFLPEDPSLPIMIGPG----- 916
QY 157 ATALLILSGI-----WQERRKNKPEVDDAEDKCN-MITENGIPSDPLDMKGILM 209
DB 917 -----SGIAPRSFWQQL-----GEIENTWPSCENTMLSCETIIPSCNSMESC 964
QY 210 MPS 212
DB 965 MPS 967

RESULT 2
ID SYR_SULTO STANDARD; PRT; 623 AA.
AC Q971X1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
GN ARGS OR ST1258.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OC NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
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RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama H., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka K., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Koshida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain 7.";
RL DNA Res 8:123-140(2001).
CC -|- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
CC diphosphate + L-arginyl-tRNA(Arg).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: Belongs to class-1 aminoacyl-tRNA synthetase family.
CC
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC ENBL; AP000985; BAB66299.1; -.
DR HAMAP; MF_00123; -. 1.
DR InterPro; IPR001278; Arg_tRNA-synt_1C.
DR InterPro; IPR008909; tRNA-synt_1C.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00750; tRNA-synt_1d; 1.
DR Pfam; PF05746; tRNA-synt_1d_C; 1.
DR PRINTS; PR01038; TRNASYNTHARG.
DR TIGRPFAMs; TIGR00456; arGS; 1.
DR PROSITE; PS00178; AA_tRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 116 126 "HIGH" REGION.
FT SITE 623 AA; 71692 MW; A24645D096B038B CRC64;
SQ SEQUENCE 623 AA; 71692 MW; A24645D096B038B CRC64;

Query Match 8.3%; Score 91; DB 1; Length 623;
Best Local Similarity 22.1%; Pred. No. 1.1;
Matches 45; Conservative 31; Mismatches 44; Indels 84; Gaps 12;

QY 45 NEELYFKAMVA-----FSMRKVPNREATEISHVLLCNVQVSFWFVVTDPKNEHTLP 99
DB 82 NESEFLKLIPTNPFEDXGIEKIQKQPVVVEH-----TSANPIHPLRVG 125
QY 100 EVQSAI-----RMVKR---INNAFLNDQ-----TLEFLKI--PSILAPMDPSVP 141
DB 126 HLRNALIGDVIARMLKARGHEVNTRFYNDAGRQVAILTLGYLLGBEN---PPRDEKID 182
QY 142 IWIIIFGVIFCI--IIVAI-----ALLILSGIWQRKRNKEP 176
DB 183 QWI---GVIAITNIIIEINQLKELSSNEEYRQKISKIDELISLAG---KHREKYP 235
QY 177 -----SEVDDAEDKCNMI 190
DB 236 EIPDKLADEISKIENIEKIQNII 259

RESULT 3
ID CAD8_MOUSE STANDARD; PRT; 799 AA.
AC P97291;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Caderlin-8 precursor.
GN CDH8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=97174321; PubMed=9022055;
 RA Korematsu K., Redies C.;
 RT "Restricted expression of cadherin-8 in segmental and functional
 RL subdivisions of the embryonic mouse brain.";
 Dev. Dyn. 208:178-189(1997).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 5 cadherin domains.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X95600; CAA64857.1; -;
 DR HSSP; P15116; INCI;
 DR MGD; MGI:107434; Cdh8.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; cadherin; 5.
 DR PRINTS; PF01049; Cadherin_C_term; 1.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 61 POTENTIAL.
 FT CHAIN 62 799 CADHERIN-8.
 FT DOMAIN 62 621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 799 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 62 167 CADHERIN 1.
 FT DOMAIN 168 276 CADHERIN 2.
 FT DOMAIN 277 391 CADHERIN 3.
 FT DOMAIN 392 494 CADHERIN 4.
 FT DOMAIN 495 616 CADHERIN 5.
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 544 544 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 799 AA; 88200 MW; 0E35FEAD563C7F76 CRC64;
 Query Match 8.2%; Score 90; DB 1; Length 799;
 Best Local Similarity 21.4%; Pred. No. 1.8;
 Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;
 QY 13 HAEICPGAGNAYKVLRIATLGDYAWDT-----NEEYLFKAMVAFSMEKVPN 63
 Db 432 HTLERFQFNADGKITATPDLRELSTVHNTIATERNHSQISRPVAVKVLVDV-N 490
 QY 64 REATEIS---HVLIC-----NTQVSFWFVVDPSKNH-----TLPAVEGSAIRMK 109
 Db 491 DNAPEPASEYEAPLCEKNGKPGQVITVSA-MDKDPGNGHFPLYSLPVMWNPFTIKK 549
 QY 110 NRINNAFFL-----NDQTEFLKIPSTLA-----PMDPSVPVWIIIFG----- 148
 Db 550 NEDNSILAKNGFNKQKQVILLPIVISDSGNPPLSSTSTITIRVCGSNDGVQSCN 609
 QY 149 -----VFICIIIVATALLSGIWMQRKRNKEPSEVDADKCNMT 191
 Db 610 VEAVVLPGLSMGALIAILACIILLVIVLFF--VTLRRHN-EPLIKKDDVDRENIIR 666
 QY 192 IEN 194
 ;;

Db 667 YDD 669
 RESULT 4
 ID CAD8_RAT STANDARD; PRT; 799 AA.
 AC 054800; 054801;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cadherin-8 precursor.
 GN Cdh8.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain;
 RX MEDLINE=98190518; PubMed=9521872;
 RA Kido M., Obata S., Tanihara H., Rochelle J.M., Seldin M.P.,
 RA Taketani S., Suzuki S.T.;
 RL "Molecular properties and chromosomal location of cadherin-8.";
 Genomics 48:186-194(1998).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=054800-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=054800-2; Sequence=VSP_000638, VSP_000639;
 CC -!- SIMILARITY: Contains 5 cadherin domains.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB010436; BAA24452.1; -;
 DR EMBL; AB010437; BAA24453.1; -;
 DR HSSP; P15116; INCI.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; cadherin; 5.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal; Alternative splicing.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 61 POTENTIAL.
 FT CHAIN 62 799 CADHERIN-8.
 FT DOMAIN 62 621 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 622 642 POTENTIAL.
 FT DOMAIN 643 799 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 62 167 CADHERIN 1.
 FT DOMAIN 168 276 CADHERIN 2.
 FT DOMAIN 277 391 CADHERIN 3.
 FT DOMAIN 392 494 CADHERIN 4.
 FT DOMAIN 495 616 CADHERIN 5.
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 544 544 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 514 532 IQTYSAMDKDPKNGHFL -> NISMLLIILNMFVYNCFLV
FT N (in isoform 2).
FT /FTID-VSP 300638.
FT VARSPLIC 533 799 Missing (in isoform 2).
FT /FTID-VSP 300639.
SQ SEQUENCE 799 AA; 88332 MW; F01D145A9066CB6 CRC64;

Query Match 8.2%; Score 90; DB 1; Length 799;
Best Local Similarity 21.4%; Pred. No. 1.8;
Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;

QY 13 HAELOCPGAENAFKVLRSIRLTALGDKAYAWDT-----NEEYLFKAMVAFSNRYKVPN 63
DB 432 HTDLERQFNADGDKITLATPLDRELSVWHNISIIATEIRNHSQISRPVPAIKVLDV-N 490

QY 64 REATEIS---HVLLC-----NVTQVSFWFVTDPSKNH-----TLPAVEQSAIRMK 109
DB 491 DNAPEFSEYBAFLCENKPGQVIGTVA-MKDDPKNGHFFLSLLPEWNNENFTIKK 549

QY 110 NRINNAFL-----NDQTLFLKIPSTLA-----PPMDPSVPIWIIIFG----- 148
DB 550 NEDNLSILAKHNGENRQKQVYLLPIVSDGNFPLSTLTIRVCGSGDGVQSCN 609

QY 149 -----VFCHIIIVAIALLHLSGIWQRKKKPESEVDDAEDKCNMIT 191
DB 610 VEPYVLPITGLSMGALIAIACILLVIVLFP--VTLRRHKN-BPLIIKKDDVDRENIIR 666

QY 192 IEN 194
DB 667 YDD 669

RESULT 5
ITAB HUMAN STANDARD; PRT; 1025 AA.
AC P53708;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrin alpha-8.
GN ITGA8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95286701; PubMed=7768999;
RA Schnapp L.M., Breuss J.M., Ramos D.M., Sheppard D., Pytela R.;
RT *Sequence and tissue distribution of the human integrin alpha 8
RT subunit: a beta 1-associated alpha subunit expressed in smooth muscle
RT cells.*;
RL J. Cell Sci. 108:537-544 (1995).
CC -!- FUNCTION: INTEGRIN ALPHA-8/BETA-1 IS A RECEPTOR FOR FIBRONECTIN
CC AND CYTOTACTIN. IT RECOGNIZES THE SEQUENCE R-G-D IN ITS LIGANDS.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA
CC SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A
CC DISULFIDE BOND. ALPHA-8 ASSOCIATES WITH BETA-1.
CC -!- SUBCELLULAR LOCATION: type 1 membrane protein.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN SMOOTH MUSCLE AND
CC SMOOTH MUSCLE-LIKE CONTRACTILE CELLS.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L36531; AAA93514.1; -

DR HSSP; P06756; LJV2.
DR Genew; HGNC:6144; ITGA8.
DR MIM; 604063.
DR GO; GO:0008305; C:integrin complex; TAS.
DR GO; GO:0004895; P:cell adhesion receptor activity; NAS.
DR GO; GO:0016337; P:cell-cell adhesion; NAS.
DR GO; GO:0007160; P:cell-matrix adhesion; NAS.
DR InterPro; IPR000413; Integrin_alpha.
DR Pfam; PF01839; FG-GAP 4.
DR Pfam; PF00357; integrin_A; 1.
DR PRINTS; PR01185; INTEGRINA.
DR SMART; SM00191; Int_alpha; 6.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW Repeat; Calcium.
FT CHAIN 1 868 INTEGRIN ALPHA-8 HEAVY CHAIN (POTENTIAL).
FT CHAIN 869 1025 INTEGRIN ALPHA-8 LIGHT CHAIN (POTENTIAL).
FT DOMAIN 1 974 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 975 995 POTENTIAL.
FT DOMAIN 996 1025 CYTOPLASMIC (POTENTIAL).
FT REPEAT 16 79 FG-GAP 1.
FT REPEAT 95 160 FG-GAP 2.
FT REPEAT 161 225 FG-GAP 3.
FT REPEAT 226 279 FG-GAP 4.
FT REPEAT 280 345 FG-GAP 5.
FT REPEAT 346 405 FG-GAP 6.
FT REPEAT 409 463 FG-GAP 7.
FT CA_BIND 291 299 POTENTIAL.
FT CA_BIND 421 429 POTENTIAL.
FT SITE 417 419 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 58 68 BY SIMILARITY.
FT DISULFID 112 133 BY SIMILARITY.
FT DISULFID 149 162 BY SIMILARITY.
FT DISULFID 469 480 BY SIMILARITY.
FT DISULFID 486 542 BY SIMILARITY.
FT DISULFID 603 609 BY SIMILARITY.
FT DISULFID 675 688 BY SIMILARITY.
FT DISULFID 829 886 INTERCHAIN (BY SIMILARITY).
FT DISULFID 891 896 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 563 563 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 681 681 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 699 699 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 715 715 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 742 742 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 858 858 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 885 885 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 967 967 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1025 AA; 113612 MW; 58BB6B2C00CF7B93 CRC64;

Query Match 8.1%; Score 89.5; DB 1; Length 1025;
Best Local Similarity 20.2%; Pred. No. 2.8;
Matches 34; Conservative 35; Mismatches 40; Indels 59; Gaps 8;

QY 20 GAENAFKVLRSIRLTALGDKAYAWDTNEEYLFKAMVAFSNRYKVPNREATEISHVLLCNVTQ 79
DB 903 GGSAV---LKVRSRLWAHTFLQKNDPVALASLVSEVKCMPTD----- 945

QY 80 RVSEFVFTDPSKNHTLP--AVEQVSQAIRMKNRINNAFLNDQTLFLKIPSTLAPPMD 137
DB 946 -----QPAK---LPEGSIATKSV-----IWAT--PNVS 969

QY 138 PSVPWIIIFGVICIIIVAIALLIL--SGIWQRKKKPESEVDDAE 193
DB 970 FSIPLWVILLAILGLLVLTALTLALWKCGFFDRARPQ3--DMTDRE 1015

RESULT 6
 ID CAD8 HUMAN STANDARD; PRT; 799 AA.
 AC P5286; Q9ULB2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cadherin-8 precursor.
 GN CDH8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10861224;
 RA Shimoyama Y., Teujimoto G., Kitajima M., Katori M.,
 RT "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins.";
 RT Biochem. J. 349:159-167(2000).
 RL [2]
 RN SEQUENCE OF 7-799 FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Heidmark R.L., St John T., Suzuki S.,
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin.";
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RX TISSUE=Petal brain;
 RA MEDLINE=91283540; PubMed=2059658;
 RT Suzuki S., Sano K., Tanihara H.,
 RT "Diversity of the cadherin family: evidence for eight new cadherins
 RL in nervous tissue.";
 RL Cell Regul. 2:261-270(1991).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB035305; BAB7419.1;
 DR EMBL; L34060; AAA35628.1; ALT_INIT.
 DR HSSP; P15116; INCIJ.
 DR Genew; HGNC:1767; CDH8.
 DR MIN; 603008;
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002033; Cadherin_C_term.
 DR Pfam; PF00028; cadherin; 5.
 DR Pfam; PF01049; Cadherin_C_term; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal.

FT	SIGNAL	1	29	POTENTIAL.
FT	PROPEP	30	61	POTENTIAL.
FT	CHAIN	62	799	CADHERIN-8.
FT	DOMAIN	62	621	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	622	642	POTENTIAL.
FT	DOMAIN	643	799	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	62	167	CADHERIN 1.
FT	DOMAIN	168	276	CADHERIN 2.
FT	DOMAIN	277	331	CADHERIN 3.
FT	DOMAIN	392	494	CADHERIN 4.
FT	DOMAIN	495	616	CADHERIN 5.
FT	CARBOHYD	33	33	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	57	57	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	188	188	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	463	463	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	473	473	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	544	544	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CONFLICT	355	355	V -> D (IN REF. 2 AND 3).
FT	CONFLICT	647	647	H -> HQ (IN REF. 2 AND 3).
SQ	SEQUENCE	799 AA;	88253 MW;	9B119B86039C6A0A CRC64;

Query Match 8.1%; Score 89; DB 1; Length 799;
 Best Local Similarity 21.4%; Pred. NO. 2.3;
 Matches 52; Conservative 34; Mismatches 91; Indels 66; Gaps 11;

QY	13	HAELOCPCGAENAFKVLRLSIRLTALGDKAYAWDT-----NNEYLKAMVAFSMKVPN	63
DB	432	HTDLERQFNINADGKITLATPLDRLSVWHNITILATEIRNHSQISRPVVALKVLVDV-N	490
QY	64	REATEIS-----HVLCC-----NVTQVSPFWFVVDPSKNH-----TLPAVEVQSARIMNK	109
DB	491	DNAPEFASVEAFPCENGKPGQVIQTVSA-MDKDPKNGHYFLYSLLEPMVNNPFTICK	549
QY	110	NRINNAFFL-----NDQTLFLFKIPSTLA-----PPMDSPVPIWIIIFG-----	148
DB	550	NEDNSLSILAKNGFRQKQEVYLLIISDSGNPLSSTSLTIRVCGSNDGVVQSCN	609
QY	149	-----VIFCIIVAIALLILSGIWQRKKNKPESEVDDAEDKCNMT	191
DB	610	VEAYVLPICGLSMGALITAILAILLVIVLP--VTLRHKH-EPLIKDDEVDRENIIR	666
QY	192	IEN 194	
DB	667	YDD 669	

RESULT 7
 CD44_MOUSE STANDARD; PRT; 778 AA.
 AC P15379; Q05732; Q61395; Q62060; Q62061; Q62062; Q62063; Q62408;
 AC Q62409; Q64296; Q99J14; Q9QX8;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE CD44 antigen precursor (Phagocytic glycoprotein I) (PSP-1) (HUTCH-I)
 DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
 DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
 DE (LY-24).
 GN CD44.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 6; 7 AND 12).
 RX STRAIN=DBA/2; TISSUE=Lung;
 RC MEDLINE=93107170; PubMed=1469058;
 RA He Q., Lesley J., Hyman R., Ishihara K., Kincade P.W.,
 RT "Molecular isoforms of murine CD44 and evidence that the membrane
 RT proximal domain is not critical for hyaluronate recognition.";
 RL J. Cell Biol. 119:1711-1719(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 13).

RX MEDLINE=90038499; PubMed=2681416;
RA Zhou D.F.H., Ding J.F., Pickar L.J., Bargatzke R.F., Butcher E.C.,
RA Goeddel D.V.,
RT "Molecular cloning and expression of Pgp-1. The mouse homolog of the
RT human h-CAM (Hermes) lymphocyte homing receptor.",
RL J. Immunol. 143:3390-3395(1989).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 13).
RX MEDLINE=90046829; PubMed=2682651;
RA Nottenburg C., Rees G., St John T.,
RA "Isolation of mouse CD44 cDNA: structural features are distinct from
RT the primate cDNA.",
RL Proc. Natl. Acad. Sci. U.S.A. 86:8521-8525(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 11).
RX MEDLINE=20318634; PubMed=10859330;
RA Wittig B.M., Johansson B., Zoeller M., Schwaerzler C., Guenther U.,
RA "Abrogation of experimental colitis correlates with increased
RT apoptosis in mice deficient for CD44 variant exon 7 (CD44v7).",
RL J. Exp. Med. 191:2053-2064(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 13).
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.X.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 13).
RX STRAIN=C57BL/6J; TISSUE=Embryo;
RA MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaio I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
RA Gramond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Leshard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Resole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Mizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kigawa I.,
RA Miyazaki A., Sakai D., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,

RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.",
RL Nature 420:563-573(2002).
RN [7]
RP SEQUENCE OF 8-778 FROM N.A. (ISOFORM 13).
RX MEDLINE=90094420; PubMed=2403553;
RA Wolffe E.J., Gause W.C., Pelfrey C.M., Holland S.M., Steinberg A.D.,
RA August J.T.,
RT "The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell
RT surface antigen and proteoglycan core/link proteins.",
RL J. Biol. Chem. 265:341-347(1990).
RN [8]
RP SEQUENCE OF 224-637 FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).
RX STRAIN=GR;
RA MEDLINE=93219085; PubMed=8464707;
RA Toelg C., Hofmann M., Herrlich P., Ponta H.,
RT "Splicing choice from ten variant exons establishes CD44
RT variability.",
RL Nucleic Acids Res. 21:1225-1229(1993).
RN [9]
RP SEQUENCE OF 224-637 FROM N.A. (ISOFORM 9).
RX STRAIN=BALB/C;
RA MEDLINE=93286043; PubMed=8509353;
RA Sreaton G.R., Bell M.V., Bell J.I., Jackson D.G.,
RT "The identification of a new alternative exon with highly restricted
RT tissue expression in transcripts encoding the mouse Pgp-1 (CD44)
RT homing receptor. Comparison of all 10 variable exons between mouse,
RT human, and rat.",
RL J. Biol. Chem. 268:12235-12238(1993).
RN [10]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11).
RX STRAIN=Swiss Webster;
RA MEDLINE=96355396; PubMed=8702806;
RA Yu Q., Toole B.P.,
RT "A new alternatively spliced exon between v9 and v10 provides a
RT molecular basis for synthesis of soluble CD44.",
RL J. Biol. Chem. 271:20603-20607(1996).
CC -1- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=13;
CC Name=1;
CC IsoId=P15379-14; Sequence=Displayed;
CC Name=2;
CC IsoId=P15379-7; Sequence=VSP_007329;
CC Name=3;
CC IsoId=P15379-8; Sequence=VSP_007330;
CC Name=4; Synonyms=M2;
CC IsoId=P15379-4; Sequence=VSP_007331;
CC Name=5;
CC IsoId=P15379-9; Sequence=VSP_007332;
CC Name=6; Synonyms=M3;
CC IsoId=P15379-5; Sequence=VSP_005326;
CC Name=7; Synonyms=M4;
CC IsoId=P15379-6; Sequence=VSP_005327;
CC Name=8;
CC IsoId=P15379-10; Sequence=VSP_007330, VSP_007334;
CC Name=9;
CC IsoId=P15379-11; Sequence=VSP_007332, VSP_007335;
CC Name=10;
CC IsoId=P15379-12; Sequence=VSP_007336, VSP_007337;
CC Name=11;
CC IsoId=P15379-13; Sequence=VSP_007338, VSP_007339;
CC Name=12; Synonyms=M1;
CC IsoId=P15379-3; Sequence=VSP_005328;
CC Name=13; Synonyms=M0;
CC IsoId=P15379-2; Sequence=VSP_005329;
CC -1- PTM: N-glycosylated (by similarity).
CC -1- PTM: O-glycosylated; contains chondroitin sulfate glycans which
CC can be more or less sulfated (by similarity).

DE (Heparan sulfate proteoglycan) (HAM1 antigen).
GN CD44.
CS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=LVG; TISSUE=Alveolar macrophage;
RA Paulauskis J.D., Kobzik L., Gerard C., Katlier M., Godleski J.J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1; IsoId=Q60522-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q60522-2; Sequence=VSP_005322;
CC -!- PTM: N-glycosylated (By similarity).
CC -!- PTM: O-glycosylated; Contains chondroitin sulfate glycans which
CC can be more or less sulfated (By similarity).
CC -!- PTM: Phosphorylated; activation of PKC results in the
CC dephosphorylation of Ser-395 (constitutive phosphorylation site),
CC and the phosphorylation of Ser-361 (By similarity).
CC -!- SIMILARITY: Contains 1 link domain.
CC -----
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CC -----
DR EMBL; U10880; AAC13767.1; -;
DR EMBL; U10881; AA19316.1; -;
DR HSPF; P98066; ITSG.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PR00918; Link; 1.
DR SMART; SM00445; Link; 1.
DR PROSITE; PS01241; LINK; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;
KW Proteoglycan; Signal; Alternative splicing;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 22
FT CHAIN 23 431
FT DOMAIN 23 338
FT TRANSMEM 339 359
FT DOMAIN 360 431
FT POTENTIAL 50 121
FT CYTOPLASMIC (POTENTIAL).
FT LINK.
FT ARG/LYS-RICH (BASIC).
FT STEM.
FT PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT PHOSPHORYLATION (BY PKC) (PARTIAL) (BY
FT SIMILARITY).
FT PHOSPHORYLATION (PARTIAL) (BY
FT SIMILARITY).
FT N-LINKED (GLNAC. . .) (POTENTIAL).
FT N-LINKED (GLNAC. . .) (POTENTIAL).
FT N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27
FT CARBOHYD 59 59
FT CARBOHYD 102 102

FT CARBOHYD 112 112 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLNAC. . .) (POTENTIAL).
FT TRSGGKGRGGGLPKDATTSLGGYTHYPETWENGLTPV
FT VARSPLIC 222 291
FT TAAKTVGTEVTVAEDSKFNVDGSLPG -> R (in
FT isoform 2).
FT /FTID=VSP_005322.
SQ SEQUENCE 431 AA; 46807 MW; 4300263E0C6BEA6A CRC64;
Query Match 7.8%; Score 86; DB 1; Length 431;
Best Local Similarity 22.0%; Pred. No. 2.1;
Matches 24; Conservative 22; Mismatches 29; Indels 34; Gaps 3;
QY 130 STLAPMDSVPIWIIIFGIFCIIVAIALLISGIWRRR-----XN 173
DB 326 TTSRPGKFKPIPEWLI---VLASLALAILAVCIANRRRGQKKKLVINGNGKVED 382
QY 174 KPSSEVDDAEDKCNMTIENGIPSDP-----LDMKGGI 207
DB 383 RKPSELNGEASKSQENVLNKPSETPDQFMTADETRNLQNVDMKIGV 431
RESULT 10
CD44 RAT
ID CD44 RAT STANDARD; PRT; 503 AA.
AC P26051; Q99021.
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-I) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
DE (LY-24).
DE GN CD44.
OS Rattus norvegicus (Rat).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BDIX; TISSUE=Pancreas;
RX MEDLINE=91191552; PubMed=1707342;
RA Guenther U., Hofmann M., Rudy W., Reber S., Zoeller M.,
RA Hausmann I., Matzku S., Wenzel A., Ponta H., Herrlich P.;
RT "A new variant of glycoprotein CD44 confers metastatic potential to
RT rat carcinoma cells";
RL Cell 65:13-24 (1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stevens J.W., Midura R.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=2; Synonyms=Long, Meta-1;
CC IsoId=P26051-1; Sequence=Displayed;
CC Name=1; Synonyms=Short;
CC IsoId=P26051-2; Sequence=VSP_005330;
CC -!- PTM: N-glycosylated (By similarity).
CC -!- PTM: O-glycosylated; Contains chondroitin sulfate glycans which
CC can be more or less sulfated (By similarity).
CC -!- PTM: Phosphorylated; activation of PKC results in the
CC dephosphorylation of Ser-467 (constitutive phosphorylation site),
CC and the phosphorylation of Ser-433 (By similarity).
CC -!- SIMILARITY: Contains 1 link domain.
CC -----

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DR EMBL; M61875; AAA53532.1; -
DR EMBL; M61874; AAA53534.1; -
DR EMBL; U52179; AAA97915.1; -
DR EMBL; U46957; AAA92920.1; -
DR PIR; B38745; B38745.
DR HSP; P98066; ITSG.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR00538; Link.
DR Pfam; PF00193; XLiik; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;
KW Proteoglycan; Signal; Alternative splicing;
KW Pyroglutamate; Signal; Alternative splicing;
FT SIGNAL 1 21
FT CHAIN 22 503
FT DOMAIN 22 410
FT TRANSMEM 411 503
FT DOMAIN 432 503
FT DOMAIN 51 123
FT DOMAIN 154 162
FT DOMAIN 228 410
FT MOD_RES 22 22
FT DISUFID 56 122
FT DISUFID 80 100
FT MOD_RES 433 433
FT MOD_RES 467 467
FT CARBOHYD 28 28
FT CARBOHYD 60 60
FT CARBOHYD 103 103
FT CARBOHYD 114 114
FT CARBOHYD 124 124
FT CARBOHYD 266 266
FT CARBOHYD 274 274
FT CARBOHYD 306 306
FT VARSPIC 224 385
FT RNSTAARGENWTEQPPFNNHXYQDEESTPHATSTTWADP
FT NSTFRAATQKRWKFNWQGNKPPPSDSHVTEGTASA
FT HNNHPQRWTTQEDVSWTDFDPFISHPMQGHQTESK
FT -> SDGDSMDPRGGFDVTTHGSELA (in isoform
FT 1).
FT FTId-VSP_005330.
FT CONFLICT 74 74 R -> S (IN REF. 2).
FT SEQUENCE 503 AA; 55945 MW; F8489D009B04E22 CRC64;
Query Match 7.8%; Score 86; DB 1; Length 503;
Best Local Similarity 20.7%; Pred. No. 2.5;
Matches 23; Conservative 24; Mismatches 30; Indels 34; Gaps 3;
QY 128 IPTSLAPPMDPSFIMIIIGVIFCIIVAILLSGIWQR- - - - - 171
Db 396 VTTSTGPARPQIPFELII- - - - - LASLALAILAVCIANRSRRCCQKKLVINSNGTV 452
QY 172 KKEPEVDVDAEKCENMIPIENGIPSD- - - - - PLDMKGGI 207
Db 453 EDRKPELNGEASKSQEWHVANKETETPDQFWTADETNLQSDVMKLGIV 503
RESULT 11
FLIF_BACSU

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ID AC P23447;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DR Flagellar M-ring protein.
GN FLIF OR BSU16210.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91285431; PubMed=1905667;
RA Zuberi A.R., Ying C., Bischoff D.S., Ordal G.W.;
RT "Gene-protein relationships in the flagellar hook-basal body complex
RT of Bacillus subtilis: sequences of the flgB, flgC, flgE and
RT flf genes."
RL Gene 101:23-31(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lepidine A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parto V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche S., Rose M., Sadaie Y.,
RA Sato T., Scantian E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 355-536 FROM N.A.
RX STRAIN=168;
RX MEDLINE=91258343; PubMed=1828465;
RA Albertini A.M., Caramori T., Crabb W.D., Scoffone F., Galizzi A.;
RT "The flia locus of Bacillus subtilis is part of a large operon coding
RT for flagellar structures, motility functions, and an ATPase-like
RT polypeptide."
RL J. Bacteriol. 173:3573-3579(1991).
CC -!- FUNCTION: The M ring may be actively involved in energy
CC transduction.
CC -!- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
CC FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
CC MOUNTED ON A CENTRAL ROD. THE M RING IS INTEGRAL TO THE INNER
CC MEMBRANE OF THE CELL AND MAY BE CONNECTED TO THE FLAGELLAR ROD
CC VIA THE S RING. THE S (SUPRAMEMBRANE RING) LIES JUST DISTAL TO
CC THE M RING. THE L AND P RINGS LIE IN THE OUTER MEMBRANE AND THE
CC PERIPLASMIC SPACE, RESPECTIVELY.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; membrane-associated.
CC -!- SIMILARITY: Belongs to the flif family.

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CC -----
CC ENBL; M54965; -; NOT ANNOTATED_CDS.
CC ENBL; Z99112; CAB13494.1; -;
CC ENBL; X56049; CAA339520.1; -;
CC DR Subtilisin; BG10240; flif.
CC DR InterPro; IPR000067; FlgMing FLIF.
CC DR InterPro; IPR006182; YscJ FLIF.
CC DR Pfam; PF01514; YscJ FLIF; 1.
CC DR PRINTS; PR01009; FLGMRINGFLIF.
CC DR TIGRFAMs; TIGR00206; flif; 1.
CC DR Flagellum; Membrane, Complete proteome.
CC KW SEQUENCE 536 AA; 5930 MW; 21110D4C7CF1927A CRC64;
CC
CC Query Match 7.7%; Score 84.5; DB 1; Length 536;
CC Best Local Similarity 19.9%; Pred. No. 3.7;
CC Matches 39; Conservative 36; Mismatches 68; Indels 53; Gaps 8;
CC
CC Qy 9 VTAHAEALCQCAENAEKVRISRTALGDKAYADTNEEYLFKAWAFSMRKVPNREATE 68
CC Ds 352 VNRHKET-----ASPKYKVR-----DLGIQVNVPEPDARNTASLTERQDD 393
CC Qy 69 ISHVLICNVTVQSFVFWVTPDSKNHTLPAVEVQSAIRNMKNRINNAFFLNDQTLLEFLKI 128
CC Ds 394 IQKIL--STVVRTS---LDKDETQNLSADINNKIVSVQPFDGKVLNDTNEE--- 444
CC Qy 129 PSTLAPPMDPVPVW-ITIFGVIFCIITVALILGILGWRRRNKVPESVDDAKDCE 187
CC Ds 445 -----SSGIPLWAYIVGGVLAATVLIIMLI-----RKRAQEDFEFEYEVE-- 487
CC
CC Qy 188 NMITIENGIPSDPLDM 203
CC Ds 488 -----VPOEPINL 495
CC
CC RESULT 12
CC ID PTPJ HUMAN STANDARD; PRT; 1337 AA.
CC AC Q12913; Q15255; Q8NEM2;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DE protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
CC DE (HPTP eta) (Protein-tyrosine phosphatase receptor type J) (Density
CC DE enhanced phosphatase-1) (DEP-1) (CD148 antigen).
CC GN PTPRJ OR DEPI
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC R2 SEQUENCE FROM N.A.
CC RX MEDLINE=95024024; PubMed=7937872;
CC RA Gestman A., Yang Q., Tonks N.K.;
CC RT "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,
CC RT is enhanced with increasing cell density."
CC RL Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
CC RN [2]
CC R2 SEQUENCE FROM N.A.
CC RX MEDLINE=95086212; PubMed=7994032;
CC RA Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;
CC RT "Molecular cloning, characterization, and chromosomal localization of
CC RT a novel protein-tyrosine phosphatase, HPTP eta."
CC RL Blood 84:4186-4194(1994).
CC RN [3]
RP SEQUENCE OF 33-1337 FROM N.A., AND VARIANTS COLON CANCER CYS-214 AND
RP PRO-276.
RP TISSUE=Colon;
RX MEDLINE=22084388; PubMed=12089527;
RA Ruiyenkamp C.A.L., van Wezel T., Zanon C., Stassen A.P.M., Vicek C.,
RA Csikos T., Klous A.M., Tripodis N., Perrakis A., Boerrigter L.,
RA Groot P.C., Lindeman J., Moci W.J., Meijer G.A., Scholten G.,
RA Dauwerse H., Faces V., van Zandwijk N., van Omen G.J.B., Demant P.;
RT Ptpj is a candidate for the mouse colon-cancer susceptibility locus
RT Sccl and is frequently deleted in human cancers.";
RL Nat. Genet. 31:295-300(2002).
CC -!- FUNCTION: May contribute to the mechanism of contact inhibition of
CC cell growth.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate. Type I membrane protein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: N- and O-glycosylated.
CC -!- DISEASE: Defects in PTPRJ are found in cancers of colon, lung, and
CC breast.
CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC -!- SIMILARITY: Contains 5 fibronectin type III domains.
CC -!- DATABASE: NAME=PROJ; NOTE=CD guide CD148 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/proj/cd/cd148.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; U10886; AAB36687.1; -;
CC EMBL; D37781; BAA07035.1; -;
CC DR ENBL; AF387844; AAM69432.1; JOINED.
CC DR ENBL; AF387823; AAM69432.1; JOINED.
CC DR ENBL; AF387824; AAM69432.1; JOINED.
CC DR ENBL; AF387825; AAM69432.1; JOINED.
CC DR ENBL; AF387826; AAM69432.1; JOINED.
CC DR ENBL; AF387827; AAM69432.1; JOINED.
CC DR ENBL; AF387828; AAM69432.1; JOINED.
CC DR ENBL; AF387829; AAM69432.1; JOINED.
CC DR ENBL; AF387830; AAM69432.1; JOINED.
CC DR ENBL; AF387831; AAM69432.1; JOINED.
CC DR ENBL; AF387832; AAM69432.1; JOINED.
CC DR ENBL; AF387833; AAM69432.1; JOINED.
CC DR ENBL; AF387834; AAM69432.1; JOINED.
CC DR ENBL; AF387835; AAM69432.1; JOINED.
CC DR ENBL; AF387836; AAM69432.1; JOINED.
CC DR ENBL; AF387837; AAM69432.1; JOINED.
CC DR ENBL; AF387838; AAM69432.1; JOINED.
CC DR ENBL; AF387839; AAM69432.1; JOINED.
CC DR ENBL; AF387840; AAM69432.1; JOINED.
CC DR ENBL; AF387841; AAM69432.1; JOINED.
CC DR ENBL; AF387842; AAM69432.1; JOINED.
CC DR ENBL; AF387843; AAM69432.1; JOINED.
CC DR PIR; I38670; I38670.
CC DR HSSP; P18052; 11YFO.
CC DR Genew; HGNC:9673; PTPRJ.
CC DR MIN; 600925; -;
CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
CC DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.
CC DR GO; GO:007267; P:cell-cell signaling; TAS.
CC DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC DR GO; GO:0007159; P:transmembrane receptor protein tyrosine kin. .; TAS.
CC DR InterPro; IPR008957; FN III-like.
CC DR InterPro; IPR003961; FN III.
CC DR InterPro; IPR000387; TYR_phosphatase.
CC DR Pfam; PF00041; En3; 6.
CC DR Pfam; PF00102; Y_phosphatase; 1.
CC DR PRINTS; PR00700; PTPRJPHPTASE.
CC DR SMART; SM00060; FN3; 8.

FT	DOMAIN	1154	1162	POLY-LEU.
FT	DOMAIN	1174	1177	POLY-ARG.
FT	CA_BIND	488	496	POTENTIAL.
FT	CA_BIND	551	559	POTENTIAL.
FT	CA_BIND	613	621	POTENTIAL.
FT	DISULFID	76	83	BY SIMILARITY.
FT	DISULFID	121	139	POTENTIAL.
FT	DISULFID	129	159	POTENTIAL.
FT	DISULFID	659	668	BY SIMILARITY.
FT	DISULFID	674	729	BY SIMILARITY.
FT	DISULFID	781	787	BY SIMILARITY.
FT	DISULFID	881	893	BY SIMILARITY.
FT	CARBOHYD	82	82	N-LINKED (GLCNAC. .)
FT	CARBOHYD	95	95	N-LINKED (GLCNAC. .)
FT	CARBOHYD	291	291	N-LINKED (GLCNAC. .)
FT	CARBOHYD	331	331	N-LINKED (GLCNAC. .)
FT	CARBOHYD	358	358	N-LINKED (GLCNAC. .)
FT	CARBOHYD	449	449	N-LINKED (GLCNAC. .)
FT	CARBOHYD	462	462	N-LINKED (GLCNAC. .)
FT	CARBOHYD	528	528	N-LINKED (GLCNAC. .)
FT	CARBOHYD	642	642	N-LINKED (GLCNAC. .)
FT	CARBOHYD	594	594	N-LINKED (GLCNAC. .)
FT	CARBOHYD	857	857	N-LINKED (GLCNAC. .)
FT	CARBOHYD	894	894	N-LINKED (GLCNAC. .)
FT	CARBOHYD	973	973	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1032	1032	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1040	1040	N-LINKED (GLCNAC. .)
FT	VARIANT	433	433	V -> M.
FT	VARIANT	524	524	/FTid=VAR_009889.
FT	VARIANT	972	972	R -> L.
FT	VARIANT	1003	1003	/FTid=VAR_009890.
FT	VARIANT	1030	1030	L -> P.
FT	VARIANT	1094	1094	/FTid=VAR_009891.
FT	VARIANT	1030	1030	I -> M.
FT	VARIANT	1094	1094	/FTid=VAR_009892.
FT	VARIANT	1030	1030	Missing.
FT	VARIANT	1094	1094	/FTid=VAR_009893.
FT	VARIANT	1030	1030	L -> V.
FT	VARIANT	1094	1094	/FTid=VAR_009894.
SQ	SEQUENCE	1189 AA; 133609 MW; 60303C08A44CD52 CRC64;		

Query Match 7.4%; Score 82; DB 1; Length 1189;

Best Local Similarity 21.4%; Pred. No. 16; Mismatches 40; Indels 74; Gaps 11;

Matches 42; Conservative 40; Mismatches 74; Indels 74; Gaps 11;

QY	7	PLVTAIHAELCQPGAEAFKVLRSIRLTALGDK-----AYAWDTNVEYLFKAMVAFSKVKY	61
Db	998	PPHIGIMMKITPIATRSNELLKLRDLPTDEVANTSNCIWNSTERYR-PTPVEEDLRR	1056
QY	62	P-----NREATEISHVLLCNV-----TORVSE-----WVVTDPSKNHTLPAVEVQS-AI	105
Db	1057	POLNHSNSDVVSIN-----CNRLVPNQEINPHLLGNLW-----RSKALKYKSKMI	1104
QY	106	RMN---KNRINNAPFLNDQTLFLKIPSTLAPPMDPSVPIWIIIFGVIICIIIVAIALLI	162
Db	1105	MVNAALQRFHSPIFREED-PSRQIVFEISKQEDWQVPIWIIIVGSTLGLLLALLAVLA	1163
QY	163	L--SGIWQRRRNKEP	176
Db	1164	EWLGGFFSARRREP	1179

RESULT 15

LEU3_PHOLL	STANDARD;	PRT;	363 AA.
ID	LEU3_PHOLL		
AC	Q7N128;		
DT	15-MAR-2004 (Rel. 43, Created)		
DT	15-MAR-2004 (Rel. 43, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)		
DE	(IMDH) (3-IPM-DH).		
GN	LEUB OR PLU3674.		
OS	Photorhabdus luminescens (subsp. laumondii).		

OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Photorhabdus.
OC	NCBI_taxid=141679;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=TT01;
RX	MEDLINE=22957627; PubMed=14528314;
RA	Duchaud B., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA	Taouit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-P.,
RA	Dassa E., Deroose R., Derzelle S., Preysinet G., Gaudriault S.,
RA	Medigue C., Lanois A., Powell K., Siguer P., Vincent R., Wingate V.,
RA	Zouine M., Glaser P., Boemare N., Danchin A., Kuntz F.,
RT	"The genome sequence of the entomopathogenic bacterium Photorhabdus
RT	luminescens.";
RL	Nat. Biotechnol. 21:1307-1313(2003).
CC	- FUNCTION: Catalyzes the oxidation of 3-carboxy-2-hydroxy-4-
CC	methylpentanoate (3-isopropylmalate) to 3-carboxy-4-methyl-2-
CC	oxopentanoate. The product decarboxylates to 4-methyl-2
CC	oxopentanoate.
CC	- CATALYTIC ACTIVITY: 3-carboxy-2-hydroxy-4-methylpentanoate +
CC	NAD(+) = 3-carboxy-4-methyl-2-oxopentanoate + NADH.
CC	- PATHWAY: Leucine biosynthesis; third step.
CC	- SUBUNIT: Homodimer (By similarity).
CC	- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC	- SIMILARITY: Belongs to the isocitrate and isopropylmalate
CC	dehydrogenases family. LeuB subfamily 1.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL: BX571871; CAE16047.1; -
DR	PhotoList; plu3674; -
DR	HMAP; RF_01033; -; 1.
DR	PROSITE; PS00470; IDH_IMDH; 1.
KW	Oxidoreductase; Leucine biosynthesis; NAD; Complete proteome.
SQ	SEQUENCE 363 AA; 39510 MW; 23126184A20FEAEC CRC64;

Query Match 7.4%; Score 81.5; DB 1; Length 363;

Best Local Similarity 25.0%; Pred. No. 4.4; Mismatches 47; Conservative 24; Mismatches 54; Indels 63; Gaps 10;

QY	32	RTALGKAVAMDNTNBYLFK-----AMVAF-SMRKVPNRATEISHVLLCNVTQVRSFW-P	85
Db	152	REGQGYERAFDTEVYRFEIERIARAFESAKRSNK-----VTSIDKANVLOSSVLWRE	207
QY	86	VVTDPSKNHTLPAVEVQSALRMKNRINNAPFLNDQTLFLKIPSTLAPPMDPSVPIWII	145
Db	208	VVTEIARAY--PDVEI-----NHMYIDNATMQLIKDPSQ-----	239
QY	146	IFGVIFCIITVAIALILSGIWQRRRNKEPSEVDDAEDKCNEMITENG-IPSDPLDMK	204
Db	240	-FDVMLCSNIFG-----DILSDECA-MITGSMGLPSASLNEK	275
QY	205	GGIIMMPS	212
Db	276	GGIIMMPS	283

Search completed: April 1, 2004, 16:26:55
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2004, 16:23:49 ; Search time 45 Seconds
(without alignments)
1486.441 Million cell updates/sec

Title: US-09-997-641-387

Perfect score: 1102

Sequence: 1 MLWLLFFLVTAHAEICQPG.....ENGIPSDPLMKGGILWMP 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp Vertebrate.*
- 14: sp Unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1073	97.4	222	4 Q9HBJ8	Q9HBJ8 homo sapien
2	928	84.2	222	11 Q9ESG4	Q9ESG4 mus musculus
3	921	83.6	222	11 Q9ESG3	Q9ESG3 rattus norv
4	376	34.1	804	4 Q9UFZ6	Q9UFZ6 homo sapien
5	376	34.1	805	4 Q9NRA7	Q9NRA7 homo sapien
6	376	34.1	816	4 Q86WT0	Q86WT0 homo sapien
7	373	33.8	805	4 Q9BYF1	Q9BYF1 homo sapien
8	361	32.8	805	11 Q8R010	Q8R010 mus musculus
9	357	32.4	265	11 Q9D836	Q9D836 mus musculus
10	357	32.4	798	11 Q99N71	Q99N71 mus musculus
11	100	9.1	1053	5 Q81AQ8	Q81AQ8 plasmodium
12	97.5	8.8	1086	5 O18428	O18428 geodia cydo
13	96.5	8.8	543	11 Q8C0H7	Q8C0H7 mus musculus
14	96.5	8.8	1012	11 O70304	O70304 mus musculus
15	95.5	8.7	1406	13 Q9W6V5	Q9W6V5 gallus gall
16	93.5	8.5	929	5 Q9VR32	Q9VR32 drosophila

ALIGNMENTS

RESULT 1

ID	Q9HBJ8	PRELIMINARY	PRT	222 AA
AC	Q9HBJ8			
DT	01-MAR-2001 (TREMELrel. 16, Created)			
DT	01-MAR-2001 (TREMELrel. 16, Last sequence update)			
DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)			
DE	Kidney-specific membrane protein NX-17 (Hypothetical protein) (NX17 protein)			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21264468; PubMed=11278314;			
RA	Zhang H., Wada J., Hida K., Tsuchiyama Y., Hiragushi K., Shikata K., Wang H., Lin S., Kanwar Y.S., Makino H.;			
RT	"Collectrin, a Collecting Duct-specific Transmembrane Glycoprotein, Is a Novel Homolog of ACE2 and Is Developmentally Regulated in Embryonic Kidneys."			
RL	J. Biol. Chem. 276:17132-17139(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Colon;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Straussberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.;			

Q8CE84 mus musculus
Q7QC3 mus musculus
Q8C449 mus musculus
Q8BRK4 mus musculus
Q8WUP8 rattus norv
Q8CE61 arabidopsis
Q76326 drosophila
Q9U6E1 strongyloce
Q8QU36 tiv-like mi
Q8OX37 mus musculus
Q8C001 mus musculus
Q8C375 mus musculus
Q8GHJ4 aeromonas p
Q9FK00 arabidopsis
Q9W4T9 drosophila
Q8KXC0 chlorobium
Q8OX09 rattus norv
Q8W779 rattus norv
Q9M3D7 arabidopsis
Q8Y15 homo sapien
Q9N9Y9 drosophila
Q97174 drosophila
Q9N7S7 homo sapien
Q9HMC3 homo sapien
Q9FGB3 arabidopsis
Q9JVK7 neisseria m
Q8WYI8 homo sapien
O42598 xenopus lae
O02344 caenorhabdi

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=Bone marrow, Colon, and Kidney;
RA Strausberg R.;
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF229179; AAG09466.1; -
DR EMBL; BC015099; AAH15099.1; -
DR EMBL; BC014317; AAH14317.1; -
DR EMBL; BC050606; AAH50606.1; -
RW Hypothetical protein.
SQ SEQUENCE 222 AA; 25335 MW; 52C0ED522134ED05 CRC64;

Query Match 97.4%; Score 1073; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.7e-105;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLFFLVTAIHAELCPGNAFVKRLSIRALGDKAYAWDTNEEYLFKAWAFSMRK 60
Db 1 MLLFFLVTAIHAELCPGNAFVKRLSIRALGDKAYAWDTNEEYLFKAWAFSMRK 60
Qy 61 VPNRATEISHVLLCNVTFQVRSFVVTDPDSKNHTLPAVEQSAIRNNKRNINNAFLND 120
Db 61 VPNRATEISHVLLCNVTFQVRSFVVTDPDSKNHTLPAVEQSAIRNNKRNINNAFLND 120
Qy 121 QTLEFLKIPSTLAPPMDSPVPIIIFGVIFCIIVAIALLILSGIWRORRNKEPSEVD 180
Db 121 QTLEFLKIPSTLAPPMDSPVPIIIFGVIFCIIVAIALLILSGIWRORRNKEPSEVD 180
Qy 181 DAEDKCNMTIENGIPSDPLDMKGG 206
Db 181 DAEDKCNMTIENGIPSDPLDMKGG 206

RESULT 2
Q9ESG4
ID Q9ESG4 PRELIMINARY; PRT; 222 AA.
AC Q9ESG4
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Kidney-specific membrane protein NX-17 (0610008J07Rik protein).
GN NX17 OR 0610008J07R1X.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR;
RX MEDLINE=99362608; PubMed=10432394;
RA Zhang H., Wada J., Kanwar Y.S., Tsuchiyama Y., Hiragushi K., Hida K.,
RA Shikata K., Makino H.;
RT "Screening for genes up-regulated in 5/6 nephrectomized mouse
RT kidney.";
RL Kidney Int. 56:549-558(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217651;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukumishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,

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RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
RA Brewster M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Li X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RN SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178085; AAG09306.1; -
DR EMBL; AK002337; BAB22022.1; -
DR EMBL; BC049912; AAH49912.1; -
DR MGI; MGI:1926234; NX17.
SQ SEQUENCE 222 AA; 25070 MW; C07E732CE92935A9 CRC64;

Query Match 84.2%; Score 928; DB 11; Length 222;
Best Local Similarity 84.5%; Pred. No. 6e-90;
Matches 174; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MLLFFLVTAIHAELCPGNAFVKRLSIRALGDKAYAWDTNEEYLFKAWAFSMRK 60
Db 1 MLLFFLVTAIHAELCPGNAFVKRLSIRALGDKAYAWDTNEEYLFKAWAFSMRK 60
Qy 61 VPNRATEISHVLLCNVTFQVRSFVVTDPDSKNHTLPAVEQSAIRNNKRNINNAFLND 120
Db 61 VPNRATEISHVLLCNVTFQVRSFVVTDPDSKNHTLPAVEQSAIRNNKRNINNAFLND 120
Qy 121 QTLEFLKIPSTLAPPMDSPVPIIIFGVIFCIIVAIALLILSGIWRORRNKEPSEVD 180
Db 121 QTLEFLKIPSTLAPPMDSPVPIIIFGVIFCIIVAIALLILSGIWRORRNKEPSEVD 180
Qy 181 DAEDKCNMTIENGIPSDPLDMKGG 206
Db 181 DAEDKCNMTIENGIPSDPLDMKGG 206

RESULT 3
Q9ESG3
ID Q9ESG3 PRELIMINARY; PRT; 222 AA.
AC Q9ESG3;

```

DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DE Kidney-specific membrane protein NK-17.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=99362608; PubMed=10432394;
 RA Zhang H., Wada J., Kanwar Y.S., Tsuchiyama Y., Hiragushi K., Hida K.,
 RA Shikata K., Makino H.;
 RT "Screening for genes up-regulated in 5/6 nephrectomized mouse
 RT kidney".
 RL Kidney Int. 56:549-558(1999).
 DR EMBL: AF178086; AAGO9507.1; -. 7F4E166AE34F855 CRC64;
 SQ SEQUENCE 222 AA; 25226 MW; 7F4E166AE34F855 CRC64;

 Query Match 83.6%; Score 921; DB 11; Length 222;
 Best Local Similarity 84.5%; Pred. No. 3.3e-89;
 Matches 174; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

 QY 1 MLWLFFLVTAHAEICQGAENAFKVRISITLGDKAYADTNEEYLFKAWAFSMRK 60
 DB 1 MLWLFFLVTAHAEICQGAENAFKVRISITLGDKAYADTNEEYLFKAWAFSMRK 60
 QY 61 VNREATEISHVLLCNVTVQSVFVVDPSKNHTLPVAVQSAIRMNKRNINNAFFLND 120
 DB 61 VNREATEISHVLLCNVTVQSVFVVDPSKNHTLPVAVQSAIRMNKRNINNAFFLND 120
 QY 121 QTLFLKIPSTLAPPDPSVPIIIFGVIFCIIVAIALLISGIWQRRRNKPKPSEVD 180
 DB 121 HTLEFLKIPSTLAPPDPSVPIIIFGVIFCIIVAIALLISGIWQRRRNKPKPSEVD 180
 QY 181 DAEDKCNMTTNGIPSPDLMKGG 206
 DB 181 DAEDKCNMTTNGIPSPDLMKRG 206

 RESULT 4
 Q9UFZ6 PRELIMINARY; PRT; 804 AA.
 ID Q9UFZ6
 AC Q9UFZ6
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DE Hypothetical protein (Fragment).
 GN DKFPA34A014.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Wamburt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL110224; CAB53682.1; -.
 DR PIR: T14762; T14762.
 DR MEROPS: M02.006; -.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001548; Peptidase M2.
 DR Pfam: PF01401; Peptidase M2; 1.
 DR PRINTS: PR00791; PEPTIDTASEA.
 DR PRODOM: PD004184; Peptidase M2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Hypothetical protein.

FT NON TER 1
 SQ SEQUENCE 804 AA; 92340 MW; 91FF391074CB5DA9 CRC64;

 Query Match 34.1%; Score 376; DB 4; Length 804;
 Best Local Similarity 47.9%; Pred. No. 8.2e-31;
 Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

 QY 19 PGAENAFKRLSIRITLGDKAYADTNEEYLFKAWAFSMR---KVENREAT-EISHVL 73
 DB 611 PYAQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVNQNILFGEEDVR 670
 QY 74 LCNVTVQSVFVVDPSKNHTLPVAVQSAIRMNKRNINNAFFLNDQTLFLKIPSTL 132
 DB 671 VANLKPRISFNFVTAPQVSDIIIPRTEVEKAIAMRSRINDAFLNDNSLEFLGIQPTL 730
 QY 133 APPMDPSVPIIIFGVIFCIIVAIALLISGIWQRRRNKPKS 177
 DB 731 GPNQPPSIVLIVGVGVGVVGVILFTIGIEDRKKKNKARS 775

 RESULT 5
 Q9NRA7 PRELIMINARY; PRT; 805 AA.
 ID Q9NRA7
 AC Q9NRA7
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DE Angiotensin converting enzyme-like protein (ACE-related
 DE carboxypeptidase ACE2) (Angiotensin I converting enzyme
 DE (Peptidyl-dipeptidase A) 2).
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphoma;
 RA Turner A.J.;
 RT "A Human Homolog of Angiotensin Converting Enzyme - Cloning and
 RT Functional Expression As A Captopril-Insensitive Carboxypeptidase".
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Donoghue M., Hsieh P., Baronas E., Godbout K., Gosselin M.,
 RA Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,
 RA Breitbart R.E., Acton S.;
 RT "A novel ACE-related carboxypeptidase (ACE2) converts angiotensin I to
 RT angiotensin-1-9".
 RL Circ. Res. 0:0-0(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
 RA Ahearn M.O., Kuldane S.A., Rajkumar N., Toth E.J., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF241254; AAF78220.1; -.
 DR EMBL: AF291820; AAF99721.1; -.
 DR EMBL: AY217547; AAO25651.1; -.
 DR MEROPS: M02.006; -.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004180; F:carboxypeptidase activity; IEA.
 DR GO: GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001548; Peptidase M2.
 DR InterPro: IPR006025; Pept M Zn BS.
 DR Pfam: PF01401; Peptidase M2; 1.
 DR PRINTS: PR00791; PEPTIDTASEA.
 DR PRODOM: PD004184; Peptidase M2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Carboxypeptidase.

SQ SEQUENCE 805 AA; 92462 MW; 8EE6BE0A931550B8 CRC64;
Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 8.2e-31;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;
QY 19 PGAEAFKVRISIRIALGDKAYADTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
DB 612 PYAQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMRQYFLKVKQNILFGEDVR 671
QY 74 LCNVTQVSVFVVTDPDK-NHTLPAVEVQSARIMKNRINNAPFLNDOTLEFLKIPSTL 132
DB 672 VANLKPRISENFVFTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDSLEFLGIQFTL 731
QY 133 APPMDPSVPITWIIIFGVIFCIIVAIALLISGIWRRRKNKPS 177
DB 732 GPPNQPPVSIWLVFGVGMVIVGVILIFTGIRDRKKKNKARS 776
RESULT 6
Q86WTO PRELIMINARY; PRT; 816 AA.
AC Q86WTO
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to angiotensin I converting enzyme (Peptidyl-dipeptidase A) 2
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC Tissue=Testis;
RE Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC048094; AAH48094.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0001548; Peptidase M2.
DR InterPro; IPR001548; Peptidase M2.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPTIDPTASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
FT NON_TER
SQ SEQUENCE 816 AA; 93516 MW; EFBD56B3DA2EDF3 CRC64;
Query Match 34.1%; Score 376; DB 4; Length 816;
Best Local Similarity 47.9%; Pred. No. 8.3e-31;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;
QY 19 PGAEAFKVRISIRIALGDKAYADTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
DB 623 PYAQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMRQYFLKVKQNILFGEDVR 682
QY 74 LCNVTQVSVFVVTDPDK-NHTLPAVEVQSARIMKNRINNAPFLNDOTLEFLKIPSTL 132
DB 683 VANLKPRISENFVFTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDSLEFLGIQFTL 742
QY 133 APPMDPSVPITWIIIFGVIFCIIVAIALLISGIWRRRKNKPS 177
DB 743 GPPNQPPVSIWLVFGVGMVIVGVILIFTGIRDRKKKNKARS 787
RESULT 7
Q8BYF1 PRELIMINARY; PRT; 805 AA.
AC Q8BYF1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ACE2.
GN ACE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Komatsu T.; Suzuki Y.; Sugano S.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Suzuki Y.; Watanabe M.; Sugano S.;
RT "Cloning, expression analysis and chromosomal localization of a novel
RT ACE like enzyme.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046569; BAB40370.1; -.
DR MEROPS; M02.006; -.
DR Genew; HGNC:13557; ACE2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Pept_M2n_BS.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPTIDPTASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 805 AA; 92491 MW; D2AAB4C27088EB72 CRC64;
Query Match 33.8%; Score 373; DB 4; Length 805;
Best Local Similarity 47.3%; Pred. No. 1.7e-30;
Matches 78; Conservative 33; Mismatches 48; Indels 6; Gaps 3;
QY 19 PGAEAFKVRISIRIALGDKAYADTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
DB 612 PYAQSIKVRISLKSALGDKAYENDNEMYLFRSSVAYAMRQYFLKVKQNILFGEDVR 671
QY 74 LCNVTQVSVFVVTDPDK-NHTLPAVEVQSARIMKNRINNAPFLNDOTLEFLKIPSTL 132
DB 672 VANLKPRISENFVFTAPKNVSDIIPRTEVEKAIMRSRINDAFRLNDSLEFLGIQFTL 731
QY 133 APPMDPSVPITWIIIFGVIFCIIVAIALLISGIWRRRKNKPS 177
DB 732 GPPNQPPVSIWLVFGVGMVIVGVILIFTGIRDRKKKNKARS 776
RESULT 8
Q8RO10 PRELIMINARY; PRT; 805 AA.
AC Q8RO10
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RIKEN cDNA 2010305L05 gene.
GN ACE2 OR 2010305L05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC Tissue=Kidney;
RE Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026801; AAH26801.1; -.
DR MGD; MGI:1917258; Ace2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.


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DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001548; Peptidase_M2.
DR InterPro: IPR006025; Pept_M2n_BS.
DR InterPro: IPR001680; WD40.
DR Pfam: PF01401; Peptidase_M2; 1.
DR PRINTS: PR00791; Peptidase_M2.
DR ProDom: PD004184; Peptidase_M2; 1.
DR PROSITE: PS00678; WD_REPEATS_1; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 805 AA; 92367 MW; D8B883AAC966A8D9 CRC64;

Query Match 32.8%; Score 361; DB 11; Length 805;
Best local Similarity 40.9%; Pred. No. 3.2e-29;
Matches 81; Conservative 35; Mismatches 52; Indels 30; Gaps 5;

QY 19 PGAEAFKVLRLSIRLTALGDKAYAWDTNBYLFKAMVAFPMRK-----VPNREATEI 69
DB 612 PYADQSIKVRISLKSALGANAYETNNEMFLFRSSVAYAMRYKFSIKNTVPFLE---- 667
QY 70 SHVLLCNVTQVSEFWVVTDPK-NHTLPAVEQSAIRMKNNRINNAPFLNDOTLEFLKI 128
DB 668 EDVRSVLKRVSYFFVTSPQNSVDVIPRSEVEDAIRMSGRINDVFGNDNSLEFLGI 727
QY 129 PSTLAPPMDSPVPIIIFGVCIIIVAIALLILSGIWMQRKNKEPSEVDDAEKCEN 188
DB 728 EPTLEPPYQPEVTIILIFGVWALVVGIIILVTGIGKGRKKNETKRE----- 777
QY 189 MITIENGIPSPDLPMKG 206
DB 778 ----EN--PYDSMDIGKG 789

RESULT 9
Q9D836 PRELIMINARY; PRT; 265 AA.
ID Q9D836
AC Q9D836; TISSUE=Small intestine;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Adult male small intestine cDNA, RIKEN full-length enriched library,
DE clone:2010305L05 product:ANIGOTENSIN-converting enzyme-related
DE carboxypeptidase, full insert sequence (Fragment).
GN ACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Inotani K., Iishi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.
PL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Tamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa K., Tanaka T., Matsura S., Kawai J.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
DR EMBL; AK008530; BAB25723.2; -.
DR MED; MGI:1917258; Ace2.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004246; F:peptidyl-diesterase A activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001548; Peptidase_M2.
DR Pfam: PF01401; Peptidase_M2; 1.
DR NON_TER 1
SQ SEQUENCE 265 AA; 30078 MW; 2A02B2CE3817C76C CRC64;

Query Match 32.4%; Score 357; DB 11; Length 265;
Best local Similarity 44.1%; Pred. No. 2.2e-29;
Matches 75; Conservative 33; Mismatches 48; Indels 14; Gaps 3;

QY 19 PGAEAFKVLRLSIRLTALGDKAYAWDTNBYLFKAMVAFPMRK-----VPNREATEI 69
DB 72 PYADQSIKVRISLKSALGANAYETNNEMFLFRSSVAYAMRYKFSIKNTVPFLE---- 127
QY 70 SHVLLCNVTQVSEFWVVTDPK-NHTLPAVEQSAIRMKNNRINNAPFLNDOTLEFLKI 128
DB 128 EDVRSVLKRVSYFFVTSPQNSVDVIPRSEVEDAIRMSGRINDVFGNDNSLEFLGI 187
QY 129 PSTLAPPMDSPVPIIIFGVCIIIVAIALLILSGIWMQRKNKEPSE 178
DB 188 HPTLEPPYQPEVTIILIFGVWALVVGIIILVTGIGKGRKKNETKRE 237

RESULT 10
Q99N71 PRELIMINARY; PRT; 798 AA.
ID Q99N71
AC Q99N71;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anigotensin-converting enzyme-related carboxypeptidase.
GN 2010305L05RIK OR ACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RA SEQUENCE FROM N.A.
RA Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Ymada Y.,
RA Hida M., Tanigami A., Muroi S.;
RT "Molecular cloning, mRNA expression, and chromosomal localization of
RT mouse Angiotensin-converting Enzyme-Related Carboxypeptidase.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033181; BAB40431.1; -.
DR MEROPS; M02.006; -.
DR MGD; MGI:1917258; Ace2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR GO; GO:0004246; F:peptidyl-diesterase A activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001548; Peptidase M2.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001680; WD40.
DR Pfam; PF01401; Peptidase M2; 1.
DR PRINTS; PR00791; PEPTIDTASEA.
DR ProDom; PD004184; Peptidase M2; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Carboxypeptidase.
SQ SEQUENCE 798 AA; 91943 MW; 403AEA29D55725A4 CRC64;

Query Match 32.4%; Score 357; DB 11; Length 798;
Best Local Similarity 44.1%; Pred. No. 8.3e-29;
Matches 75; Conservative 33; Mismatches 48; Indels 14; Gaps 3;

QY 19 PGENAFKVLRSIRLTALGDKAYADTNEEYLFKAWAFSMRK-----VNPREATETI 69
DB 612 PYAQSIKVRISLXALCANAYTNEMFPRSSVAYAKRKYPSIIKNGTVPPLE---- 667
QY 70 SHVLLCNVTQVSFWFVTDPSK-NHTLPAVEVQSAIRMKRNINNAFFNDOTLEFKI 128
DB 668 EDVRVSLDKPRVSFFVFFTSQNVSDVIPRSEVDAIRMGGRINDVFGINDNSLEFLGI 727
QY 129 PSTLAPPMDPSVPIWIIFGFIICIIIVAIALLISGIWQRRRNKPPSE 178
DB 728 HPTLEPPYQPPVTIWLIFGVVMAVGVIIILVTGKGRKKNETKRE 777

RESULT 11
Q81AQ8 PRELIMINARY; PRT; 1053 AA.
AC Q81AQ8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Vacuolar proton-translocating ATPase subunit A, putative.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN RA SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrall B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844507; CAD51303.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015920; P:proton transport; IEA.
DR InterPro; IPR002490; V_ATPase_sub116.
DR Pfam; PF01496; V_ATPase_sub_a_1; 1.
SQ SEQUENCE 1053 AA; 122998 MW; 8B9F2559D3FC3F08 CRC64;

Query Match 91.1%; Score 100; DB 5; Length 1053;
Best Local Similarity 21.3%; Pred. No. 0.19;
Matches 43; Conservative 31; Mismatches 72; Indels 56; Gaps 8;

QY 22 ENAFKVLRSIRLTALGDKAYADTNEEYLFKAWAFSMRKVNPREATETISHVLLC----- 75

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DB 330 EHAQGLKELRLIINDKEXALAYEYFNEIFVLINNVPEKNKSLIEEWKLPCKKXERHI 389
QY 76 -----NVTQVSFWFVTDPSK-NHTLPAVEVQSAIRMKRNINNAFFNDOTL- 123
DB 390 YANLNYFEQSDITLRCDCWYSANDEKIRHIL-----INKSSNDLVALLSKILR 441
QY 124 -----EFLK-----IPSTLAPP-----MDPSVPIWI-----IFGVIF- 153
DB 442 FNVSPPTIYIKTNEFKYSQSMVDYGVPRYGEINPAISTIIIFPFLFGIMGVGVHGLCI 501
QY 154 IIVAIALLISGIWQRRRNKKE 175
DB 502 FLFALEFLIIMNKNVKNKKNNE 523

RESULT 12
Q18428 PRELIMINARY; PRT; 1086 AA.
AC Q18428;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Integrin.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demosporangia; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN RA SEQUENCE FROM N.A.
MEDLINE-97254937; PubMed-9100369;
Pancer Z., Kruse M., Mueller I., Mueller W.B.G.;
RT On the origin of adhesion receptors of metazoa: Cloning of the
RT integrin alpha subunit cDNA from the sponge Geodia cydonium.;
RL Mol. Biol. Evol. 14:391-398(1997).
DR EMBL; X97283; CAA65943.1; -.
DR PIR; T18523; T18523.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0004895; P:cell adhesion receptor activity; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR Pfam; PF01839; FG-GAP; 3.
DR PRINTS; PR01185; INTEGRINA.
DR SMART; SM00191; Int_alpha; 4.
SQ SEQUENCE 1086 AA; 118628 MW; 269189D0364DBPA5 CRC64;

Query Match 8.8%; Score 97.5; DB 5; Length 1086;
Best Local Similarity 25.5%; Pred. No. 0.37;
Matches 36; Conservative 24; Mismatches 52; Indels 29; Gaps 6;

QY 63 NREATEISHVL-----LCNVTQVSFWFVTDPSKNTLPAVEVQSAIRMKRNINNAFFL 118
DB 963 NRQVQISAVIDERHAGIDSYTF-----PSAQ-----VEMVGSDHINESNTKD---- 1007
QY 119 NDOTLEFLKIPSTLAPP-----DPSVPIWIIFGFIICIIIVAIALLISGIWQRRRN 173
DB 1008 NNAAEFRTIPGELVVPVSGSGDDESVPVVIAPVPIIAAVIIIVVAVVLYFCGFRKN 1067
QY 174 KEPSVDDAEDKCNMTIEN 194
DB 1068 KQ-----EIEDQARENLAEN 1083

RESULT 13
Q8COH7 PRELIMINARY; PRT; 543 AA.
AC Q8COH7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Alpha 8 integrin (Fragment).
GN A1447669.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK031326; BAC27348.1; -
 DR MGD; MGI:2138946; AI447669.
 DR GO; GO:0008305; C:integrin complex; IEA.
 DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
 DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
 DR InterPro; IPR000413; Integrin_alpha.
 DR Pfam; PF00357; Integrin_A; 1.
 DR PRINTS; PR01185; INTEGRIN.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 FT NON_TER 1
 FT SEQUENCE 543 AA; 61249 MW; 430DCB3279A8FD4 CRC64;
 SQ
 Query Match 8.8%; Score 96.5; DB 11; Length 543;
 Best Local Similarity 22.0%; Pred. No. 0.2;
 Matches 37; Conservative 32; Mismatches 40; Indels 59; Gaps 8;
 QY 20 GAENAFKVLRSIRLTALGDKAYADNTNEEYLFKAMVAFSKVPNREATEISHVLLCNVTQ 79
 DB 421 GGSAV---LKVRSRLWAHTFLKRNKNDHYALASLVSEVKMPYKE----- 463
 QY 80 RVSFVFWVTDPSKNTLPA--VEVQSAIRMKNNRINNNAFFLNDQTLFLKIPSTLAPPMD 137
 DB 464 -----QPAK---LPAGSTAVKTSV-----IWAT--PNVS 487
 QY 138 PSVPFIILFGVIFCIIVAILLIL--SGIWORRRKKNKEPSEVDDAE 183
 DB 488 PSIPLVIIAILLLGLVAILTLALWKCGFFDRARPPQD--EMTDRE 533
 RESULT 14
 O70304 PRELIMINARY; PRT; 1012 AA.
 ID O70304
 AC O70304
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Integrin alpha8 (Fragment).
 GN ITG8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97207007; PubMed=9054500;
 RA Muller U., Wang D., Denda S., Meneses J.J., Pedersen R.A.,
 RA Reichardt L.F.;
 RT "Integrin alpha8 beta1 is critically important for epithelial-
 RT mesenchymal interactions during kidney morphogenesis.";
 RL Cell 88:603-613 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98217301; PubMed=9548928;
 RA Denda S., Muller U., Crossin K.L., Brickson H.P., Reichardt L.F.;
 RT "Utilization of a soluble integrin-alkaline phosphatase chimera to
 RT characterize integrin alpha 8 beta 1 receptor interactions with
 RT tenascin: murine alpha 8 beta 1 binds to the RGD site in tenascin-C
 RT fragments, but not to native tenascin-C";
 RL Biochemistry 37:5464-5474 (1998).
 DR EMBL; AF041409; AAC15665.1; -
 DR HSSP; P06756; IJUV2.

DR MGD; MGI:109442; Itga8.
 DR GO; GO:0008305; C:integrin complex; IEA.
 DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
 DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
 DR InterPro; IPR000413; Integrin_alpha.
 DR Pfam; PF00357; FG-GAP; 4.
 DR Pfam; PF01839; FG-GAP; 4.
 DR PRINTS; PR01185; INTEGRIN_A; 1.
 DR PRINTS; PR01185; INTEGRIN_A.
 DR SMART; SM00191; Int_alpha; 5.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 FT NON_TER 1
 FT NON_TER 1012
 FT SEQUENCE 1012 AA; 112384 MW; 2A535AEC33867581 CRC64;
 SQ
 Query Match 8.8%; Score 96.5; DB 11; Length 1012;
 Best Local Similarity 22.0%; Pred. No. 0.43;
 Matches 37; Conservative 32; Mismatches 40; Indels 59; Gaps 8;
 QY 20 GAENAFKVLRSIRLTALGDKAYADNTNEEYLFKAMVAFSKVPNREATEISHVLLCNVTQ 79
 DB 896 GGSAV---LKVRSRLWAHTFLKRNKNDHYALASLVSEVKMPYKE----- 938
 QY 80 RVSFVFWVTDPSKNTLPA--VEVQSAIRMKNNRINNNAFFLNDQTLFLKIPSTLAPPMD 137
 DB 939 -----QPAK---LPAGSTAVKTSV-----IWAT--PNVS 962
 QY 138 PSVPFIILFGVIFCIIVAILLIL--SGIWORRRKKNKEPSEVDDAE 183
 DB 963 PSIPLVIIAILLLGLVAILTLALWKCGFFDRARPPQD--EMTDRE 1008
 RESULT 15
 Q9W6V5 PRELIMINARY; PRT; 1406 AA.
 ID Q9W6V5
 AC Q9W6V5
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Supporting-cell antigen precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=99296852; PubMed=10366616;
 RA Kruger R.P., Goodyear R.J., Legan P.K., Warchol M., Raphael Y.,
 RA Cotanche D.A., Richardson G.P.;
 RT "The supporting-cell antigen: a receptor-like protein tyrosine
 RT phosphatase expressed in the sensory epithelia of the inner ear.";
 RL J. Neurosci. 19:4815-4827 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RA Legan P.K.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ238216; CAB41885.2; -
 DR HSSP; P18052; IYFO.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 9.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 9.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolase; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 SQ SEQUENCE 1406 AA; 154213 MW; 2D609885CC0F367B CRC64;
 Query Match 8.7%; Score 95.5; DB 13; Length 1406;
 Best Local Similarity 25.0%; Pred. No. 0.81;
 Matches 31; Conservative 22; Mismatches 50; Indels 21; Gaps 4;
 QY 87 VTDPKXHTLPVAVQSAIRMKNKRNINNAFLN-----DQTLFLKIPSTLAP 134
 Db 976 IVDVKGNTMYGNYENGSLPLHSTRASVAGFTNINFTVANKINGEQSYVSFPCSEVVSL 1035
 QY 135 PMDPSVPWIIIFGVIFCIIVAIALLISG--IWQRRRNKSPSEVDDAEDKCE--NMI 190
 Db 1036 PQDPGV-----IAGAVIGCLLAILAVVAIGGYIFWRRRRKDKRNTVSPSPKIKKSKMI 1090
 QY 191 TIEN 194
 Db 1091 KVEN 1094

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